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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:10:48 ; Search time 89.0685 Seconds
(without alignments)
2104.671 Million cell updates/sec

Title: US-10-627-886-26

Perfect score: 2465

Sequence: 1 MDATTGDTALQAVKQMAT.....GANIAGFTKVDVAKQAGV 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2465	100.0	476	16 US-10-627-886-26	Sequence 26, Appl
3	2465	100.0	487	9 US-09-070-844-24	Sequence 24, Appl
4	2465	100.0	487	16 US-10-627-886-24	Sequence 24, Appl
5	2465	100.0	512	9 US-09-070-844-4	Sequence 4, Appl
6	2465	100.0	512	16 US-10-627-886-4	Sequence 4, Appl
7	2465	100.0	526	9 US-09-070-844-2	Sequence 2, Appl
8	2465	100.0	526	16 US-10-627-886-2	Sequence 2, Appl
9	1309	53.1	445	15 US-10-282-122A-66687	Sequence 6687, A
10	1300.5	52.8	444	18 US-10-988-943-43	Sequence 43, Appl
11	1297.5	52.6	444	15 US-10-282-122A-65129	Sequence 65129, A

12	1294.5	52.5	444	15 US-10-282-122A-66041	Sequence 66041, A
13	1294.5	52.5	444	15 US-10-275-026A-152	Sequence 152, App
14	1287.5	52.2	449	15 US-10-282-122A-67538	Sequence 67538, A
15	1281	52.0	445	15 US-10-369-493-13947	Sequence 13947, A
16	1259	51.1	454	15 US-10-369-493-9839	Sequence 9839, Ap
17	1257.5	51.0	462	15 US-10-282-122A-45200	Sequence 45200, A
18	1239.5	50.3	448	15 US-10-282-122A-57310	Sequence 57310, A
19	1239.5	50.3	448	18 US-10-953-901-338	Sequence 338, App
20	1238	50.2	449	14 US-10-260-877-90	Sequence 90, Appl
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23	1230	49.9	449	15 US-10-282-122A-66870	Sequence 66870, A
24	1214	49.2	448	15 US-10-282-122A-74024	Sequence 74024, A
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29	1205.5	48.9	424	15 US-10-282-122A-48442	Sequence 48442, A
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35	1195.5	48.5	448	15 US-10-369-493-8215	Sequence 8215, Ap
36	1194	48.4	438	15 US-10-369-493-10621	Sequence 10621, A
37	1191	48.3	447	15 US-10-282-122A-60243	Sequence 60243, A
38	1191	48.3	447	20 US-11-073-550-80	Sequence 80, Appl
39	1185	48.1	447	9 US-09-738-626-6982	Sequence 6982, Ap
40	1184	48.0	447	20 US-11-073-550-82	Sequence 82, Appl
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43	1180.5	47.9	458	15 US-10-282-122A-60810	Sequence 60810, A
44	1180	47.9	447	15 US-10-369-493-295	Sequence 295, App
45	1178	47.8	447	15 US-10-282-122A-72769	Sequence 72769, A

ALIGNMENTS

RESULT 1

US-09-070-844-26
; Sequence 26, Application US/09070844
; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155

TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-070-844-26

Query Match 100.0%; Score 2465; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.1e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIPMKDPEQEFMQAVREV 60
DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIPMKDPEQEFMQAVREV 60
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DB 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
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DB 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQCSFMTE 180
QY 181 LQRHSYVDVPAGDIGVGAREIGYLFQYKRIITKNYTGVLTPKGQYGGSSIRPEATGY 240
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DB 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360
DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360
QY 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420
DB 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420
QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476
DB 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

RESULT 2

US-10-627-886-26
Sequence 26, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Saliwanchik & Saliwanchik
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886

FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UP-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-627-886-26

Query Match 100.0%; Score 2465; DB 16; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.1e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIPMKDPEQEFMQAVREV 60
DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIPMKDPEQEFMQAVREV 60
QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
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DB 181 LQRHSYVDVPAGDIGVGAREIGYLFQYKRIITKNYTGVLTPKGQYGGSSIRPEATGY 240
QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
DB 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
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DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360
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DB 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

RESULT 3
US-09-070-844-24
Sequence 24, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Saliwanchik & Saliwanchik
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: Florida
;; COUNTRY: USA
;; ZIP: 32606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/070,844
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/725,596
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Whitlock, Ted W.
;; REGISTRATION NUMBER: 36,965
;; REFERENCE/DOCKET NUMBER: UF155
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (904) 375-8100
;; TELEFAX: (904) 372-5800
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 487 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-070-844-24

Query Match 100.0%; Score 2465; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.3e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQQEFMQAVREV 71

QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRTITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 72 AVSLQPVFEKRPPELLPIFKQIVPEPVRTITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131

QY 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDPDKGSDAEVMPFCQSFMT 180
DB 132 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDPDKGSDAEVMPFCQSFMT 191

QY 181 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTIKNTYTGVLTPKGOEYGGSEIRPEATGY 240
DB 192 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTIKNTYTGVLTPKGOEYGGSEIRPEATGY 251

QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 300
DB 252 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 311

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAFPCCATQNEIDH 360
DB 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAFPCCATQNEIDH 371

QY 361 DAELLIKHGCQYVVEGANPSTNEAIIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMS 420
DB 372 DAELLIKHGCQYVVEGANPSTNEAIIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMS 431

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DB 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKQAGAV 487

RESULT 4

US-10-627-886-24

;; Sequence 24, Application US/10627886
;; Publication No. US20040128710A1
;; GENERAL INFORMATION:
;; APPLICANT: Schmidt, Robert R.
;; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
;; RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE
;; DEHYDROGENASES AND METHODS OF USE
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Saliwanchik & Saliwanchik
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: Florida
;; COUNTRY: USA
;; ZIP: 32606-6669
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/627,886
;; FILING DATE: 24-Jul-2003
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/070,844
;; FILING DATE: 01-MAY-98
;; APPLICATION NUMBER: 08/725,596
;; FILING DATE: 03-OCT-96
;; APPLICATION NUMBER: 08/541,033
;; FILING DATE: 06-OCT-95
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lloyd, Jeff
;; REGISTRATION NUMBER: 35,589
;; REFERENCE/DOCKET NUMBER: UF-155CD3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (352) 375-8100
;; TELEFAX: (352) 372-5800
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 487 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-627-886-24

Query Match 100.0%; Score 2465; DB 16; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.3e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQQEFMQAVREV 60
DB 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQQEFMQAVREV 71

QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRTITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 72 AVSLQPVFEKRPPELLPIFKQIVPEPVRTITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131

QY 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDPDKGSDAEVMPFCQSFMT 180
DB 132 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDPDKGSDAEVMPFCQSFMT 191

QY 181 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTIKNTYTGVLTPKGOEYGGSEIRPEATGY 240
DB 192 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTIKNTYTGVLTPKGOEYGGSEIRPEATGY 251

QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 300
DB 252 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 311

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAFPCCATQNEIDH 360

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Db 312 FTREQQAQVDMKKKNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAFPCCATQNEIDEH 371
QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420
Db 372 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 431
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476
Db 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 487

RESULT 5
US-09-070-844-4
; Sequence 4, Application US/09070844
; Patent No. US20020062493A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-4

Query Match 100.0%; Score 2465; DB 9; Length 512;
Best Local Similarity 100.0%; Pred. No. 5.7e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTFALQKAVQKATKAGTEGLVHGINKPNPVRQLLTIFPMKDPEQBFMQAVREV 60
Db 37 MDATTGDTFALQKAVQKATKAGTEGLVHGINKPNPVRQLLTIFPMKDPEQBFMQAVREV 96
QY 61 AVSLQPVFKRPPELLPIKQIIVEPRVITFRYSWLDNAGLQVNRGFRVQYSALGPYKG 120
Db 97 AVSLQPVFKRPPELLPIKQIIVEPRVITFRYSWLDNAGLQVNRGFRVQYSALGPYKG 156
QY 121 GLRFPSPVNLIMKFLAPFQIFKNSLTTLPMGGGKGSGDFDPKSKSDAEVMEFCQSPMTE 180
Db 157 GLRFPSPVNLIMKFLAPFQIFKNSLTTLPMGGGKGSGDFDPKSKSDAEVMEFCQSPMTE 216
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QY 181 LQRHSYVQDYPAGDIGVGAREIGYLGQYKRITKNYTGVLTPKQOEGSGSEIRPEATGY 240
Db 217 LQRHSYVQDYPAGDIGVGAREIGYLGQYKRITKNYTGVLTPKQOEGSGSEIRPEATGY 276
QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 300
Db 277 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 336
QY 301 FTREQQAQVDMKKKNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAFPCCATQNEIDEH 360
Db 337 FTREQQAQVDMKKKNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAFPCCATQNEIDEH 396
QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420
Db 397 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 456
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476
Db 457 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 512

RESULT 6
US-10-627-886-4
; Sequence 4, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; APPLICATION NUMBER: 08/725,596
; FILING DATE: 03-OCT-96
; APPLICATION NUMBER: 08/541,033
; FILING DATE: 06-OCT-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: UF-155CD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-627-886-4

Query Match 100.0%; Score 2465; DB 16; Length 512;
Best Local Similarity 100.0%; Pred. No. 5.7e-221;
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Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQEQBFMQAVREV 60
DB 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQEQBFMQAVREV 96
QY 61 AVSLQPVFEKPEPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 97 AVSLQPVFEKPEPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRFHPSVNLKIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCOSFMT 180
DB 157 GLRFHPSVNLKIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCOSFMT 216
QY 181 LQRHISYVDVPAGDIGVAREIGYLFQYKRITKNTYGLVTPKGQYGGSEIRPEATGY 240
DB 217 LQRHISYVDVPAGDIGVAREIGYLFQYKRITKNTYGLVTPKGQYGGSEIRPEATGY 276
QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQYVYEPNG 300
DB 277 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQYVYEPNG 336
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVVYVGDRRKPWELDCQVDIAFPFCATQNEIDEH 360
DB 337 FTREQLQAVQDMKKKNSARISEYKSDTAVVYVGDRRKPWELDCQVDIAFPFCATQNEIDEH 396
QY 361 DAELLIKHGCGQYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420
DB 397 DAELLIKHGCGQYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 456
QY 421 LNWTRREEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQGAV 476
DB 457 LNWTRREEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQGAV 512

RESULT 7

US-09-070-844-2
; Sequence 2, Application US/09070844
; Patent No. US2002062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-2

Query Match 100.0%; Score 2465; DB 9; Length 526;
Best Local Similarity 100.0%; Pred. No. 5.9e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQEQBFMQAVREV 60
DB 51 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQEQBFMQAVREV 110
QY 61 AVSLQPVFEKPEPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 111 AVSLQPVFEKPEPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
QY 121 GLRFHPSVNLKIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCOSFMT 180
DB 171 GLRFHPSVNLKIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCOSFMT 230
QY 181 LQRHISYVDVPAGDIGVAREIGYLFQYKRITKNTYGLVTPKGQYGGSEIRPEATGY 240
DB 231 LQRHISYVDVPAGDIGVAREIGYLFQYKRITKNTYGLVTPKGQYGGSEIRPEATGY 290
QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQYVYEPNG 300
DB 281 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQYVYEPNG 350
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVVYVGDRRKPWELDCQVDIAFPFCATQNEIDEH 360
DB 351 FTREQLQAVQDMKKKNSARISEYKSDTAVVYVGDRRKPWELDCQVDIAFPFCATQNEIDEH 410
QY 361 DAELLIKHGCGQYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420
DB 411 DAELLIKHGCGQYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 470
QY 421 LNWTRREEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQGAV 476
DB 471 LNWTRREEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQGAV 526

RESULT 8

US-10-627-886-2
; Sequence 2, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844

```

/ FILING DATE: 01-MAY-98
/ APPLICATION NUMBER: 08/725,596
/ FILING DATE: 03-OCT-96
/ APPLICATION NUMBER: 08/541,033
/ FILING DATE: 06-OCT-95
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lloyd, Jeff
/ REGISTRATION NUMBER: 35,589
/ REFERENCE/DOCKET NUMBER: UP-155CD3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 526 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-627-886-2

Query Match 100.0%; Score 2465; DB 16; Length 526;
Best Local Similarity 100.0%; Pred. No. 5.9e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALOKAVKQMATKAGTEGLVHGIKNPDVRLQLTEIFMKDPEQBFMQAVREV 60
DB 51 MDATTGDTALOKAVKQMATKAGTEGLVHGIKNPDVRLQLTEIFMKDPEQBFMQAVREV 110
QY 61 AVSLQPVFEKRPPELLPIFQKQIIEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 111 AVSLQPVFEKRPPELLPIFQKQIIEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
QY 121 GLRPHSPVNLSTIMKFLAPFQIPKNSLTTLPMGGGKGSDFDPKGSKDAEVMRFGQSPFMT 180
DB 171 GLRPHSPVNLSTIMKFLAPFQIPKNSLTTLPMGGGKGSDFDPKGSKDAEVMRFGQSPFMT 230
QY 181 LQRHSYVQDVDPAGDIGVCAREIGYLFQYKQITKNYTGVLTPKQYGGSSIRPEATGY 240
DB 231 LQRHSYVQDVDPAGDIGVCAREIGYLFQYKQITKNYTGVLTPKQYGGSSIRPEATGY 290
QY 241 GAVLFVENVLKDGBSLKGRCLVSGAGNAQVYCAELLLEKGAIVLSLSDSGYVYEPNG 300
DB 291 GAVLFVENVLKDGBSLKGRCLVSGAGNAQVYCAELLLEKGAIVLSLSDSGYVYEPNG 350
QY 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGDRRKRWELDCQVDIAPPQATQNEIDEH 360
DB 351 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGDRRKRWELDCQVDIAPPQATQNEIDEH 410
QY 361 DAELLIKHGCQVYVVGANPNSTNEAIHKYNKAGIICPCKAANAGGVAVSGLEMTQNRMS 420
DB 411 DAELLIKHGCQVYVVGANPNSTNEAIHKYNKAGIICPCKAANAGGVAVSGLEMTQNRMS 470
QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYNYVDLAAGANIAGFTTKVADAVKAQGV 476
DB 471 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYNYVDLAAGANIAGFTTKVADAVKAQGV 526

RESULT 9
US-10-282-122A-66687
/ Sequence 66687, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Lianguo
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert

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/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 66687
/ LENGTH: 445
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66687

Query Match 53.1%; Score 1309; DB 15; Length 445;
Best Local Similarity 59.2%; Pred. No. 4.5e-113;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 36 VQLLTETFMKDPQBFMQAVREVAVSLQPVFEKRPPELLP--IFKQIIEPVRVITFRVS 93
DB 5 VDAFLERLKRDPDPQBFMQAVEVLRSLWPFLEANPHYLEAGIIEIVEPERAILFRVP 64
QY 94 WLDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLSTIMKFLAPFQIPKNSLTTLPMGG 153
DB 65 WVDQGRVVRNRGFRVQYSSAIGPYKGLRPHSPVNLSTIMKFLAPFQIPKNSLTTLPMGG 124
QY 154 KGKGSDDPDKGSKDAEVMRFGQSPFMTLQRIHSYVQDVDPAGDIGVCAREIGYLFQYKRI 213
DB 125 KGKGSDDPDKGSKDAEVMRFGQSPFMTLYRHVGADLDVDPAGDIGVCAREIGYLFQYKRL 184
QY 214 TKNYTGVLTPKQYGGSSIRPEATGYGAVLFVENVLKDGBSLKGRCLVSGAGNAQY 273
DB 185 SNQFTSVLTGKLSYGGSLIRPEATGFCVYFAQEMLKDRGDPGQGVAVSGSNVAY 244
QY 274 CAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQDMKKNNNSARISEYKSDTAVYV 333
DB 245 AARKVMEGGKVIISLSDSEGTLYABAGLSDSQWBYLMELKNVRR-GRIREMABQFSLOFL 303
QY 334 DRRKRWELDCQVDIAPPQATQNEIDEHDAELLIKHGCQVYVVGANPNSTNEAIHKYNKAG 393
DB 304 EGRPPWGLAC--DIALPCATQNEIDEHDAERLLANGCVCAEGANMSTLEAVDLPLEAG 361
QY 394 IICYCPGAANAGGVAVSGLEMTQNRMSLNWTRREEVRDKLERIMKDIYDSA-MGPSRRYNY 452
DB 362 ILVAPGRKASNAGGVAVSGLEMSQNAWRLRWSEGEVDTKLHGIMQSIHHAICLLYGEQGRV 421
QY 453 DLAAGANIAGFTTKVADAVKAQGV 476
DB 422 NYVKGANIAGFTTKVADAVKAQGV 445

RESULT 10

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US-10-988-943-43
; Sequence 43, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; FILE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; TITLE OF INVENTION: COMPLEX MIXTURES.
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-43

Query Match      52.8%; Score 1300.5; DB 18; Length 444;
Best Local Similarity 57.4%; Pred. No. 2.8e-112;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 35 DVRLQLTEIFMKDPQEQEFMQAVREAVSVLQPFVFKRPPELL--PIFKQIVPEPRTVTRV 92
DB 3 DLNLTFLANLKQRPNQEPFHQAQVEVFMSLDPLPFLAKNPKYTOQSLRLERIVEPVRV 62
QY 93 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFLAFLAFLAFLAFLAFLA 152
DB 63 TWQDDKGQVQVNRGRVQVSSAIGPYKGLRPHPSVNLISIMKFLAFLAFLAFLAFLAFLAFLA 122
QY 153 GKGGSDFDPKGSKDAEVMRFQCSFMTQLQRHISYVQDVDPAGDIGVGAREIGYLFQYKKR 212
DB 123 GKGGSDFDPKGSKDAEVMRFQCSFMTQLQRHISYVQDVDPAGDIGVGAREIGYLFQYKKR 182
QY 213 ITKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCVLSGAGNVAQ 272
DB 243 YAAEKAIQLGAKVLTVSDSDGFLPFDIGMTAEQAQLAALIELKEVRE-RVATYAKEQGLQ 301
QY 332 VGDRRKPELDCQVDIAFPQATQNEIDEHDAELLIKHGQYVVEGANNPSTNEAIIHKYNK 391
DB 302 YFENQKPMGV--AAEIALPCATQNELDEEAATLLANGCYVVAEGANMSTLGAVEQFTK 359
QY 392 AGIIPCCKAANAGGAVSVGLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRY- 450
DB 360 AGIYAPGKASNAGGAVTSGLEMSQNAIRLSWTREVRDQRLFGIMQSIHESCL----KYG 415
QY 451 ----NVDLAAGANIAGFTKVADAVKAQG 474
DB 416 KVGDKVYVNGANIAGFVKVADAMLAQG 443

RESULT 11
US-10-282-122A-65129
; Sequence 65129, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65129
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65129

Query Match      52.6%; Score 1297.5; DB 15; Length 444;
Best Local Similarity 57.4%; Pred. No. 5.4e-112;
Matches 257; Conservative 70; Mismatches 106; Indels 15; Gaps 6;

QY 35 DVRLQLTEIFMKDPQEQEFMQAVREAVSVLQPFVFKRPPELL--PIFKQIVPEPRTVTRV 92
DB 3 DLNLTFLANLKQRPNQEPFHQAQVEVFMSLDPLPFLAKNPKYTOQSLRLERIVEPVRV 62
QY 93 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFLAFLAFLAFLAFLAFLA 152
DB 63 TWQDDKGQVQVNRGRVQVSSAIGPYKGLRPHPSVNLISIMKFLAFLAFLAFLAFLAFLAFLA 122
QY 153 GKGGSDFDPKGSKDAEVMRFQCSFMTQLQRHISYVQDVDPAGDIGVGAREIGYLFQYKKR 212
DB 123 GKGGSDFDPKGSKDAEVMRFQCSFMTQLQRHISYVQDVDPAGDIGVGAREIGYLFQYKKR 182
QY 213 ITKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCVLSGAGNVAQ 272
DB 183 IRNEFTSVLTGKLEWGGSLIRPEATGYGCVYFAQAMLTQNRNDSFEGKRVLSGSGNVAQ 242
QY 273 YCAELLLKGAIVLSLSDSQGYVVEPN-GFTREQLQAVODMKKKNNSARISEYKSDTAVY 331
DB 243 YAAEKAIQLGAKVLTVSDSDGFLPFDIGMTAEQAQLAALIELKEVRE-RVATYAKEQGLQ 301
QY 332 VGDRRKPELDCQVDIAFPQATQNEIDEHDAELLIKHGQYVVEGANNPSTNEAIIHKYNK 391
DB 302 YFENQKPMGV--AAEIALPCATQNELDEEAATLLANGCYVVAEGANMSTLGAVEQFTK 359
QY 392 AGIIPCCKAANAGGAVSVGLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRY- 450
DB 360 AGIYAPGKASNAGGAVTSGLEMSQNAIRLSWTREVRDQRLFGIMQSIHESCL----KYG 415
QY 451 ----NVDLAAGANIAGFTKVADAVKAQG 474
DB 416 KVGDKVYVNGANIAGFVKVADAMLAQG 443

RESULT 12
US-10-282-122A-66041
; Sequence 66041, Application US/10282122A
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66041
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-10-282-122A-66041

Query Match      52.5%; Score 1294.5; DB 15; Length 444;
Best Local Similarity 57.1%; Pred. No. 1e-111;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

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Db 3 DLNTLFLANLKQRNPQEPHQAVBEVFMSLDPLFLAKNPKYTQOSLLERIVEPERVVMFVR 62
QY 93 SWLDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAFEQIPKNSLTTLPMG 152
Db 63 TWQDDKGVQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAFEQIPKNSLTTLPMG 122
QY 153 GKGGSDFDPKGSDAEVMRFQSQFMTLORHISYVQDVPAGDIGVGAREIGYLFQGYKR 212
Db 123 GKGGSDFDPKGSDAEVMRFQSQFMTLORHISYVQDVPAGDIGVGAREIGYLFQGYKR 182
QY 213 ITKNYTVGLTPKGQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 272
Db 183 IRNEFSSVLTGKLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ 242
QY 273 YCAELLLEKGAIVLSLSDSQYVYEP-NGFTREQLQAVQDMKKNSARISEYKSDTAVY 331
Db 243 YAAEKAQLGAKVLTVDSDNSGVLFPSGMSQAALALTELKEVRRE-RVATYAKEQGLQ 301
QY 332 VGDRRKPWELDCQVDIAFPCCATQNEIDEHDAELLIKHGSCQYVVEGANMPSTNEAIHKYNK 391
Db 302 YFENQKPGV--AAEIALPCATQNELDEAAKTLANGCYVVAEGANMPSTGLGAVEQFIK 359
QY 392 AGIYCPOKAANAGGAVSGLMNTQNRMSLNWTREVRDKLERIMKDIYDSAMGPSRRY- 450
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QY 451 ----NVDLAAGANTAGTKKADAVKAQG 474
Db 416 KVGDTVNYVNGANTAGTVKVDADAMLAQG 443

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; Sequence 152, Application US/10275026A
; Publication No. US2004008770A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Christoph
; TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use
; FILE REFERENCE: GJB-6436
; CURRENT APPLICATION NUMBER: US/10/275,026A
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/GB01/02003
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: GB 0011108.8
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-10-275-026A-152

Query Match      52.5%; Score 1294.5; DB 15; Length 444;
Best Local Similarity 57.1%; Pred. No. 1e-111;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 35 DVROLLTEIFMKDPQEQEFMQAVREAVSLQPVFEKRPPELL--PIFQIIVEPERVITPRV 92
Db 3 DLNTLFLANLKQRNPQEPHQAVBEVFMSLDPLFLAKNPKYTQOSLLERIVEPERVVMFVR 62
QY 93 SWLDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAFEQIPKNSLTTLPMG 152
Db 63 TWQDDKGVQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAFEQIPKNSLTTLPMG 122
QY 153 GKGGSDFDPKGSDAEVMRFQSQFMTLORHISYVQDVPAGDIGVGAREIGYLFQGYKR 212
Db 123 GKGGSDFDPKGSDAEVMRFQSQFMTLORHISYVQDVPAGDIGVGAREIGYLFQGYKR 182
QY 213 ITKNYTVGLTPKGQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 272
Db 183 IRNEFSSVLTGKLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ 242
QY 273 YCAELLLEKGAIVLSLSDSQYVYEP-NGFTREQLQAVQDMKKNSARISEYKSDTAVY 331
Db 243 YAAEKAQLGAKVLTVDSDNSGVLFPSGMSQAALALTELKEVRRE-RVATYAKEQGLQ 301
QY 332 VGDRRKPWELDCQVDIAFPCCATQNEIDEHDAELLIKHGSCQYVVEGANMPSTNEAIHKYNK 391
Db 302 YFENQKPGV--AAEIALPCATQNELDEAAKTLANGCYVVAEGANMPSTGLGAVEQFIK 359
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Db 360 AGILYAPGKASNAGGAVATSGLEMSQNAIRLSWTREEVQDRLFGIMQSIHESCL----KYG 415
QY 451 ----NVDLAAGANTAGTKKADAVKAQG 474
Db 416 KVGDTVNYVNGANTAGTVKVDADAMLAQG 443

RESULT 14
US-10-282-122A-67538
; Sequence 67538, Application US/10282122A

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Job time : 91.0685 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:01:27 ; Search time 25.4942 Seconds
(without alignments)
1393.764 Million cell updates/sec

Title: US-10-627-886-26
Perfect score: 2465
Sequence: 1 MDATTGDTALQKAVKQMAT.....GANIAGFTKVADVAKQAGAV 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2465	100.0	476	2 US-08-541-033A-26	Sequence 26, Appl
2	2465	100.0	476	2 US-08-828-451-26	Sequence 26, Appl
3	2465	100.0	487	2 US-08-541-033A-24	Sequence 24, Appl
4	2465	100.0	487	2 US-08-828-451-24	Sequence 24, Appl
5	2465	100.0	512	2 US-08-541-033A-4	Sequence 4, Appl
6	2465	100.0	512	2 US-08-828-451-4	Sequence 4, Appl
7	2465	100.0	526	2 US-08-541-033A-2	Sequence 2, Appl
8	2465	100.0	526	2 US-08-828-451-2	Sequence 2, Appl
9	1309	53.1	450	4 US-09-252-991A-20646	Sequence 20646, A
10	1257.5	51.0	467	4 US-09-328-352-5725	Sequence 5725, Ap
11	1234.5	50.1	448	4 US-09-134-000C-3884	Sequence 3884, Ap
12	1221	49.5	448	4 US-09-583-110-4489	Sequence 4489, Ap
13	1201	48.7	447	2 US-08-886-640-3	Sequence 3, Appl
14	1200	48.7	447	3 US-08-884-235-11	Sequence 11, Appl
15	1200	48.7	447	1 US-08-370-193A-11	Sequence 11, Appl
16	1191	48.3	452	4 US-09-489-039A-7937	Sequence 7937, Ap
17	1177.5	47.8	446	4 US-09-543-681A-6657	Sequence 6657, Ap
18	1177	47.7	447	3 US-08-508-761B-6	Sequence 6, Appl
19	1147	46.5	461	3 US-09-171-337A-5	Sequence 5, Appl
20	1147	46.5	461	4 US-09-631-022-5	Sequence 5, Appl
21	1143	46.4	449	1 US-08-831-753-1	Sequence 1, Appl
22	1037.5	42.1	454	4 US-09-538-092-767	Sequence 767, App
23	1012	41.1	368	4 US-09-107-433-4041	Sequence 4041, Ap
24	788.5	32.0	298	4 US-09-248-796A-17483	Sequence 17483, A
25	552.5	22.4	420	3 US-09-134-001C-3103	Sequence 3103, Ap
26	537.5	21.8	374	4 US-09-710-279-2162	Sequence 2162, Ap
27	537	21.8	509	4 US-09-902-540-11352	Sequence 11352, A

28	519	21.1	420	3 US-09-239-303-9	Sequence 9, Appli
29	482.5	19.6	409	4 US-09-902-540-12638	Sequence 12638, A
30	476.5	19.3	421	3 US-09-239-303-2	Sequence 2, Appli
31	458.5	18.6	427	4 US-09-328-352-6130	Sequence 6130, Ap
32	441	17.9	432	4 US-09-489-039A-13935	Sequence 13935, A
33	385	15.6	87	2 US-08-461-990B-22	Sequence 22, Appl
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35	364.5	14.8	558	4 US-09-538-092-1153	Sequence 1153, Ap
36	357	14.5	87	2 US-08-461-990B-23	Sequence 23, Appl
37	357	14.5	558	4 US-09-538-092-832	Sequence 832, App
38	357	14.5	575	4 US-09-949-016-7622	Sequence 7622, Ap
39	357	14.5	575	4 US-09-949-016-7623	Sequence 7623, Ap
40	346	14.0	176	4 US-09-248-796A-17482	Sequence 17482, A
41	168	6.8	87	2 US-08-461-990B-21	Sequence 21, Appl
42	157.5	6.4	366	2 US-08-804-699-2	Sequence 2, Appli
43	139.5	5.7	356	2 US-08-461-990B-2	Sequence 2, Appli
44	132	5.4	1092	4 US-09-538-092-122	Sequence 122, App
45	131	5.3	351	4 US-09-198-452A-991	Sequence 991, App

ALIGNMENTS

RESULT 1
US-08-541-033A-26
; Sequence 26, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541.033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-541-033A-26

Query Match 100.0%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 7.2e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMQAVREV 60
DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMQAVREV 60

QY 61 AVSLOPVPEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 61 AVSLOPVPEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
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DB 121 GLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGGSDPDKGKSDAEVNRFCQSPMTE 180
QY 181 LQRHISYVQDVPAGDIGVAREIGVLFQYKRIITKNYTGVLTPKGOEYGGSEIRPEATGY 240
DB 181 LQRHISYVQDVPAGDIGVAREIGVLFQYKRIITKNYTGVLTPKGOEYGGSEIRPEATGY 240
QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 300
DB 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 300
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGRRKPWELDCQVDIAPPCATQNEIDEH 360
DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGRRKPWELDCQVDIAPPCATQNEIDEH 360
QY 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
DB 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476
DB 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476

RESULT 2

US-08-828-451-26
; Sequence 26, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5900
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-26

Query Match 100.0%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 7.2e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MDATGDTALQKAVKQMATKAGTEGLVHGIKNPDVROLLTEIFPKDPEQOEFMQAVREV 60
QY 61 AVSLOPVPEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 61 AVSLOPVPEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
QY 121 GLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGGSDPDKGKSDAEVNRFCQSPMTE 180
DB 121 GLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGGSDPDKGKSDAEVNRFCQSPMTE 180
QY 181 LQRHISYVQDVPAGDIGVAREIGVLFQYKRIITKNYTGVLTPKGOEYGGSEIRPEATGY 240
DB 181 LQRHISYVQDVPAGDIGVAREIGVLFQYKRIITKNYTGVLTPKGOEYGGSEIRPEATGY 240
QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 300
DB 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 300
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGRRKPWELDCQVDIAPPCATQNEIDEH 360
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QY 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
DB 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476
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RESULT 3
US-08-541-033A-24
; Sequence 24, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-541-033A-24

Query Match      100.0%; Score 2465; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 7.5e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 132 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSGDFDPKGKSDAEVWRFQCSFMTE 191

QY 181 LQRHISYVDVPAGDIGVGAREIGYLFQGYKRTKNYTGVLTPKGQYGGSEIRPEATGY 240
DB 192 LQRHISYVDVPAGDIGVGAREIGYLFQGYKRTKNYTGVLTPKGQYGGSEIRPEATGY 251

QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
DB 252 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 311

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAFPCCATQNEIDSH 360
DB 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAFPCCATQNEIDSH 371

QY 361 DAELLIKHGQCYVVEGANPSTNEAIIHKYNKAGIIVCPGKAANAGGAVVSGLEMTQNRMS 420
DB 372 DAELLIKHGQCYVVEGANPSTNEAIIHKYNKAGIIVCPGKAANAGGAVVSGLEMTQNRMS 431

QY 421 LNWTRREEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTTKVADAVKAQGA 476
DB 432 LNWTRREEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTTKVADAVKAQGA 487
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RESULT 4
US-08-828-451-24
; Sequence 24, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-24

Query Match      100.0%; Score 2465; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 7.5e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVROLLEIFMKDPEQOEPMQAVREV 60
DB 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVROLLEIFMKDPEQOEPMQAVREV 71

QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 72 AVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131

QY 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSGDFDPKGKSDAEVWRFQCSFMTE 180
DB 132 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSGDFDPKGKSDAEVWRFQCSFMTE 191

QY 181 LQRHISYVDVPAGDIGVGAREIGYLFQGYKRTKNYTGVLTPKGQYGGSEIRPEATGY 240
DB 192 LQRHISYVDVPAGDIGVGAREIGYLFQGYKRTKNYTGVLTPKGQYGGSEIRPEATGY 251

QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
DB 252 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 311

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAFPCCATQNEIDSH 360
DB 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAFPCCATQNEIDSH 371

QY 361 DAELLIKHGQCYVVEGANPSTNEAIIHKYNKAGIIVCPGKAANAGGAVVSGLEMTQNRMS 420
DB 372 DAELLIKHGQCYVVEGANPSTNEAIIHKYNKAGIIVCPGKAANAGGAVVSGLEMTQNRMS 431

QY 421 LNWTRREEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTTKVADAVKAQGA 476
DB 432 LNWTRREEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTTKVADAVKAQGA 487
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RESULT 5
US-08-541-033A-4
; Sequence 4, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-541-033A-4

Query Match 100.0%; Score 2465; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 8.1e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDATGDFALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPEQEFMQAVREV 60
DB 37 MDATGDFALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPEQEFMQAVREV 96
QY 61 AVSLQPVPEKPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 97 AVSLQPVPEKPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFCSFWTE 180
DB 157 GLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFCSFWTE 216
QY 181 LQRHSYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGQYGGSEIRPEATGY 240
DB 217 LQRHSYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGQYGGSEIRPEATGY 276
QY 241 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGQYVYEPNG 300
DB 277 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGQYVYEPNG 336
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGV 476
DB 457 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGV 512

RESULT 6
US-08-828-451-4
Sequence 4, Application US/08828451
Patent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-451-4

Query Match 100.0%; Score 2465; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 8.1e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDATGDFALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPEQEFMQAVREV 60
DB 37 MDATGDFALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPEQEFMQAVREV 96
QY 61 AVSLQPVPEKPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 97 AVSLQPVPEKPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFCSFWTE 180
DB 157 GLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFCSFWTE 216
QY 181 LQRHSYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGQYGGSEIRPEATGY 240
DB 217 LQRHSYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGQYGGSEIRPEATGY 276
QY 241 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGQYVYEPNG 300
DB 277 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGQYVYEPNG 336
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFPCCATQNEIDEH 360
DB 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFPCCATQNEIDEH 396
QY 361 DAELLIKHGQCVYVEGANPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420
DB 397 DAELLIKHGQCVYVEGANPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 456
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGV 476
DB 457 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGV 512

RESULT 7
US-08-541-033A-2
Sequence 2, Application US/08541033A
Patent No. 5879941
GENERAL INFORMATION:

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; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE A- AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-541-033A-2

Query Match 100.0%; Score 2465; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 8.4e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMQAVREV 60
Db 51 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMQAVREV 110
Qy 61 AVSLQPVFEKPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 111 AVSLQPVFEKPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
Qy 121 GLRHPSVNLNLSIMKFLAFEQIFKNSLTTLPMGGGKGSGDFDPKGSDAEVMRFQCSFMTE 180
Db 171 GLRHPSVNLNLSIMKFLAFEQIFKNSLTTLPMGGGKGSGDFDPKGSDAEVMRFQCSFMTE 230
Qy 181 LQRHSYVQDVPAGDIGVGAREIGYLFQGYKRITKNYTGVLTPKQEGYGSIRPEATGY 240
Db 231 LQRHSYVQDVPAGDIGVGAREIGYLFQGYKRITKNYTGVLTPKQEGYGSIRPEATGY 290
Qy 241 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 300
Db 291 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 350
Qy 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKRWELDCQVDIAPPCATQNEIDEH 360
Db 351 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKRWELDCQVDIAPPCATQNEIDEH 410
Qy 361 DAELLIKHGQCVVVEGANPSTNEAIIHKYNKAGIYCPCGAANAGVAVSGLEMTQNRMS 420
Db 411 DAELLIKHGQCVVVEGANPSTNEAIIHKYNKAGIYCPCGAANAGVAVSGLEMTQNRMS 470
Qy 421 LNWTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQGV 476
Db 471 LNWTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQGV 526
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RESULT 8
US-08-828-451-2
; Sequence 2, Application US/08028451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-2
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Query Match 100.0%; Score 2465; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 8.4e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMQAVREV 60
Db 51 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMQAVREV 110
Qy 61 AVSLQPVFEKPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 111 AVSLQPVFEKPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
Qy 121 GLRHPSVNLNLSIMKFLAFEQIFKNSLTTLPMGGGKGSGDFDPKGSDAEVMRFQCSFMTE 180
Db 171 GLRHPSVNLNLSIMKFLAFEQIFKNSLTTLPMGGGKGSGDFDPKGSDAEVMRFQCSFMTE 230
Qy 181 LQRHSYVQDVPAGDIGVGAREIGYLFQGYKRITKNYTGVLTPKQEGYGSIRPEATGY 240
Db 231 LQRHSYVQDVPAGDIGVGAREIGYLFQGYKRITKNYTGVLTPKQEGYGSIRPEATGY 290
Qy 241 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 300
Db 291 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 350
Qy 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKRWELDCQVDIAPPCATQNEIDEH 360
Db 351 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKRWELDCQVDIAPPCATQNEIDEH 410
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QY 361 DAELLIKHCQVVEGANPSTNEAIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMS 420
DB 411 DAELLIKHCQVVEGANPSTNEAIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMS 470
QY 421 LNWTRVEVRDKLERIMKDIYDSAMPSSRRYNDLAAGANIAGFTTKVADAVKAQAV 476
DB 471 LNWTRVEVRDKLERIMKDIYDSAMPSSRRYNDLAAGANIAGFTTKVADAVKAQAV 526

RESULT 9

US-09-252-991A-20646
; Sequence 20646, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20646
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20646

Query Match 53.1%; Score 1309; DB 4; Length 450;
Best Local Similarity 59.2%; Pred. No. 2.5e-115;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 36 VRLQLTEIFPKDPEQEFMQAVREAVLSIQVPEKPELLP--IPKQIPEPERVITFRVS 93
DB 10 VDAFLERLKRDPDPQEPFQAEEVLSRWPFLEANPHYLEAGIIEIVEPERALFRVP 69
QY 94 WDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTIMKFLAPEQIFKNSLTLLPMGG 153
DB 70 WDDQGRVRNRGFRVQYSSAIGPYKGLRPHPSVNLSTIMKFLAPEQIFKNSLTLLPMGG 129
QY 154 KGGSDFDPKGSDAEVRMFCQSFMTLQRIHSYVQDVPAGDIGVGAREIGVLFQYKRI 213
DB 130 KGGSDFDPKGSDAEVRMFCQSFMSLYRHYVGADLDVPAGDIGVGAREIGVLFQYKRL 189
QY 214 TKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 273
DB 190 SNQFTSVLTGKLSYGSLIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 249
QY 274 CABLLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQDMKKNNGARISEYKSDTAVTVG 333
DB 250 AARKVMGEMGVISLSDSGYVYEPNGFTREQLQAVQDMKKNNGARISEYKSDTAVTVG 308
QY 334 DRKRWELDCQVDIAFPCCATONEIDHDAELLIKHCQVVEGANPSTNEAIHKYNKAG 393
DB 309 EGRRPWGLAC--DIALPCATONELDAERLLANGCVCAEAGNMPSTLEAVDLFLEAG 366
QY 394 IYCPGKAANAGGVAVSGLEMTQNRMSLNWTRVEVRDKLERIMKDIYDSA-MGPSRRYNY 452
DB 367 IUYAPKASNAGGVAVSGLEMTQNRMSLNWTRVEVRDKLERIMKDIYDSA-MGPSRRYNY 426
QY 453 DIAAGANIAGFTTKVADAVKAQAV 476
DB 427 NVYKGANIAGFTTKVADAVKAQAV 450

RESULT 10

US-09-328-352-5725
; Sequence 5725, Application US/09328352
; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5725
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5725

Query Match 51.0%; Score 1257.5; DB 4; Length 467;
Best Local Similarity 55.9%; Pred. No. 2e-110;
Matches 256; Conservative 61; Mismatches 128; Indels 13; Gaps 5;
QY 27 LVH-----GKNPDVRLQLTEIFPKDPEQEFMQAVREAVLSIQVPEKPELLP--IP 78
DB 11 LIHYAEDRALKYNLNEFLNYVQARDPHQPEFLQAVEEVMTSLWPFIEKNPEYABOQGL 70
QY 79 KQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTIMKPLAF 138
DB 71 ERLVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTIMKPLAF 130
QY 139 EQIFKNSLTLLPMGGGKGSDFDPKGSDAEVRMFCQSFMTLQRIHSYVQDVPAGDIGV 198
DB 131 EQIFKNSLTLLPMGGGKGSDFDPKGSDAEVRMFCQSFMTLQRIHSYVQDVPAGDIGV 190
QY 199 GARIGVLFQYKRIHSYVQDVPAGDIGV 258
DB 191 GARIGVLFQYKRIHSYVQDVPAGDIGV 250
QY 259 GKRCVLSGAGNVAQYCAELILEKGAIVLSLSDSGYVYEPNGFTREQLQAVQDMKKNN 318
DB 251 KRTVLSGAGNVAQYCAELILEKGAIVLSLSDSGYVYEPNGFTREQLQAVQDMKKNN 309
QY 319 ARISEYKSDTAVTVGDRKRWELDCQVDIAFPCCATONEIDHDAELLIKHCQVVEGAN 378
DB 310 GRISFASKKHGFEYPEGKTPWHI--PVDIALPCATONELTGEDAKTLIANGVICVAEGAN 367
QY 379 MPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMSLNWTRVEVRDKLERIMK 438
DB 368 MPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMSLNWTRVEVRDKLERIMK 427
QY 439 IYDSAM--GPSRRYNYNDLAAGANIAGFTTKVADAVKAQ 474
DB 428 IHANCVRYGTKEGTVNYVDGANIAGFTTKVADAVKAQ 465

RESULT 11

US-09-134-000C-3884
; Sequence 3884, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3884
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3884

Query Match 50.1%; Score 1234.5; DB 4; Length 448;

	Best Local Similarity	55.9%;	Pred. No.	2.9e-108;	
	Matches	250;	Conservative	63;	Mismatches 123; Indels 11; Gaps 6;
Qy	36	VROLTLTIFMKDPQOEPMQAVREVAVALSQPFVKRPPELLP--IPKQIVSEPVITFRVS	93	:	:
Dd	7	VKNIQEKIHQLDQGTEVLQVDFELPTVEGFLKCNPOYIEANVLGVLIBERIPQFVRVP	66	:	:
Qy	94	WLDDAGNLQVNRRFRVYSSAIGPYKGGLRPHPSVNLISIMKPLAPEQIPIKNSLTTPLMGW	153	:	:
Dd	67	WQDDQGNHNVNRGRVYNQNSAIGPYKGLRFHPSPVNLISVMKFLEAQEIPIKNSLTGLPTGG	126	:	:
Qy	154	GKGSDFDPKGSDAEVMRFQCSFWTELQRHSYVDVPAGDIGVGAREIGVLFQGYKRI	213	:	:
Dd	127	GKGSDFDPKGSDAEVMRFQCSFWTELQKHIGSTDPAGDIGVGAREIGVLPQMYKRL	186	:	:
Qy	214	TKNVTGVLTPKQBQYGGSEIRPEATGYGANLVFENVLKDGESLKGRCLVSGAGNVAQY	273	:	:
Dd	187	RNYDAGVLTKGPLGWGWSQARTEATGYTVYFVKHLADKNDTFEGKKVAVSGSGNVAIY	246	:	:
Qy	274	CAELLLBKGAIVLSLSOGVYVEPNGTRELOLAQVDMKKKNNSARISEYKSDT--AVY	331	:	:
Dd	247	AMEKATELGATVIITCDSGSGFYVDEGI---DVALVKELKEKNRE-RISKYVETRKGATY	302	:	:
Qy	332	VGDRRKPEWLDCCQVDIAFPCCATONEIDSHDAELIALKHGCQYVVGAGNNPSTNEALHKYNK	391	:	:
Dd	303	Y-DKESVWNFTAYDIALPCATONEINEKQAAILVKNGVKVAAEGANNMPTCLEAVAVEAK	361	:	:
Qy	392	AGIIYCPGKAANAGGVAVSGLIEWTQNRMSLNWTREEVRDKLERIMKOIYDTSAMGPSRRYN	451	:	:
Dd	362	SAVIYCPGKAANAGGVAVSALEMSQNAERLAWSFEKVDGMLDQIMONITYETCRDTANEYQ	421	:	:
Qy	452	V--DLAAGANIAGTTKVADAVKAQAV	476	:	:
Dd	422	ARDNFVLGANIAGEKVAAMLGHVL	448	:	:

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RESULT 12
US-09-583-110-4489
; Sequence 4489, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4489
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4489

```

	Query Match	49.5%;	Score 1221;	DB 4;	Length 448;
	Best Local Similarity	55.7%;	Pred. No.5e-107;		
	Matches 248;	Conservative 64;	Mismatches 125;	Indels 8;	Gaps 4;
QY	36	VRQLLTIFPKMDPQQBFMQAVREVAVSLQVPFKRPDELLP--TFKQIVBERVITPRVS	93		
Dd	:	:	:	:	:
	:	:	:	:	:
8	IQSVFTVKARNGHEAEFLQAVEFFNTLEVPFKHPEYIEENTLARIETEPVVSRFP	67			
QY	94	WLDDAGNLVNRRFRFVOYSAGIPYKGLRLPHPSVNLISMKFLAFEQIKFNLSLTLPMGG	153		
Dd	:	:	:	:	:
68	WVDRDGKIQNRGRYRVNFNSAUGPYKGLRPHPTNQOILKPLGFEOIIFKNVLTLGPLTGG	127			
QY	154	KGKGSDFDPKGSDAEYNRRFCQSFWTELRHSIVYQDVPAGDIGVGAREIGYLFGQYKRI	213		

[illegible]

RESULT 13
US-08-886-640-3
; Sequence 3, Application US/08886640
; Patent No. 5998700
; GENERAL INFORMATION:
; APPLICANT: Lightfoot, David
; APPLICANT: Long, Lynn
; APPLICANT: Lightfoot, Maria V
; TITLE OF INVENTION: PLANTS CONTAINING THE *gdhA* GENE AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington

ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/886,640
 FILING DATE: 01-JUL-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/021,058
 FILING DATE: 02-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Kokulis, Paul K.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 81163/241766
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)-861-3503
 TELEFAX: (202)-822-0944
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 447 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-08-886-640-3

Query Match	48.7%	Score 1201;	DB 2;	Length 447;
Best Local Similarity	54.0%;	Pred. NO. 4.3e-105;		
Matches 241; Conservative	67;	Mismatches 128;	Indels 10;	Gaps 5


```

; LENGTH: 447 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-370-193A-11

Query Match      48.7%; Score 1200; DB 1; Length 447;
Best Local Similarity 54.0%; Pred. No. 5.4e-105;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 36 VRQLLEIFMKDEQOEFGQAVREAVASLQPVFEKPEL--LPFVKIIVEPERVITFRYS 93
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
7 LESFLNHVQKRDENQTEFAQAVREVTTLWPFLEQMPKYRQMSLLERLVEPERVIOFRVV 66
QY 94 WLDAGNLQVNRGRVQYSSAIGPYKGLRFHPSVNLISIMKFLAFQIIFKNSLTTLPMGG 153
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
67 WVDNRQIQVNRARVQFSSAIGPYKGMRFHPSVNLISILKFLGFQTFKNALTTLPMGG 126
QY 154 GKGGSDPDKGSDAEVMRFCQSFMTLQRHISYVQDVPAQDIGVGAREIGYLFQYKRI 213
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
127 GKGGSDPDKGSGEVMRFQCALMTELYRHLGADTDVPAGDIGVGGREVGFMAGMMKKL 186
QY 214 TKNYTGVLTQKQOEYGSSEIRPEATCGAVLFVENVLKDGESLKGKRCLVSGAGNVAQY 273
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
187 SNTACVFTKGSLGSGSLIRPEATGYGLVYFTEAMLKRHGMFGEMRVSVSGSGNVAQY 246
QY 274 CAELLEKGAIVLSLSDSQYVYEPNGFTREQQAVQDMKKKNNSARISEYKSDTAVVYG 333
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
247 AIEKAMEFGARVITASDSSGTVVDESGETYKEKLARLIEI-KASRDGRVADYAKEFGGLVYL 305
QY 334 DRKRWELDCQVDIAPPCATQNEIDEHDAELLIKHCQYVVEGANNPSTNEAIHKYNKAG 393
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 EGQOPWSL--PVDIALPCATQNELDVDAHQLIANGKAVAEAGANNPTTIEATLFFQQAG 363
QY 394 IIVCPGKAANAGVAVSGLEMTQNRMSLNWTRVEVPDKLERIMKDIYDSAM---GPSRRY 450
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
364 VLFAPGAANAGVATSGLEMPONAAARLGWKAQKVDARLHHIMLDIHHACVHGGEGET 423
QY 451 NYDLAAGANIAGFTKVADAVKAGAV 476
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
424 N--YVQGANIAGFVKVADAMLAQGVI 447
```

Search completed: September 8, 2005, 02:12:08
Job time : 26.4942 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:12:18 ; Search time 86.1641 Seconds
(without alignments)
2828.902 Million cell updates/sec

Title: US-10-627-886-26

Perfect score: 2465

Sequence: 1 MDATTGDTALQKAVQMAT.....GANTAGFTKADAVKAQGA 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2444	99.1	523	1 DHE4_CHLSO	P28998 chloroella s
2	1375	55.8	510	2 Q81LF7	Q81lf7 plasmodium
3	1361	55.2	1203	2 Q7RQ39	Q7rq39 plasmodium
4	1328	53.9	446	2 Q7YZU9	Q7yzu9 spironucleu
5	1327.5	53.9	449	2 Q7R3N7	Q7r3n7 giardia lam
6	1324.5	53.7	449	1 DHE4_GIALA	P28724 giardia lam
7	1309	53.1	445	2 Q9HVJ7	Q9hvj7 pseudomonas
8	1300.5	52.8	444	2 Q9JY71	Q9jy71 neisseria m
9	1294.5	52.5	444	2 Q9JT56	Q9jt56 neisseria m
10	1287.5	52.2	449	2 Q88Q23	Q88q23 pseudomonas
11	1285	52.1	445	2 Q9Z3C4	Q9z3c4 pseudomonas
12	1284.5	52.1	437	2 Q7YZU7	Q7yzu7 trichomonas
13	1279.5	51.9	470	2 Q96940	Q96940 plasmodium
14	1279.5	51.9	470	2 Q81LT0	Q81lt0 plasmodium
15	1265	51.3	442	2 Q9TXS8	Q9txs8 plasmodium
16	1264	51.3	442	2 Q9GTX5	Q9gtx5 plasmodium
17	1257	51.0	465	2 Q6S143	Q6s143 uncultured
18	1253.5	50.9	536	2 Q7RGT5	Q7rgt5 plasmodium
19	1250.5	50.7	448	2 Q8G6L0	Q8g6l0 bifidobacte
20	1250.5	50.7	455	2 Q8GE72	Q8ge72 ruminococcu
21	1249.5	50.7	447	2 Q6FD67	Q6fd67 acinetobact
22	1241.5	50.4	448	2 Q8XK85	Q8xk85 clostridium
23	1240.5	50.3	449	2 Q8S4J6	Q8s4j6 streptococc
24	1239.5	50.3	448	2 Q835G2	Q835g2 enterococcu
25	1238	50.2	449	1 DHE4_HAEIN	P37793 haemophilus
26	1236.5	50.2	449	2 Q8DYV7	Q8dyv7 streptococc
27	1234	50.1	447	2 Q61083	Q61083 trypanosoma
28	1231.5	50.0	462	2 Q6SW57	Q6sw57 manheimia
29	1230.5	49.9	449	2 Q8DUL2	Q8dul2 streptococc
30	1230	49.9	449	2 Q9CPJ4	Q9cpj4 pasteurella
31	1225.5	49.7	444	1 DHE3_BACTN	P94598 bacteroides

32	1225	49.7	448	2 Q9AIW1	Q9aiw1 streptococc
33	1214.5	49.3	444	1 DHE4_PRERU	P95544 prevotella
34	1214	49.2	448	2 Q8DPG0	Q8dpg0 streptococc
35	1212	49.2	448	2 Q97QB4	Q97qb4 streptococc
36	1210.5	49.1	458	2 Q9KB34	Q9kb34 bacillus ha
37	1206.5	48.9	447	2 Q7VSN6	Q7vsn6 bordetella
38	1205.5	48.9	424	2 Q9RTN9	Q9rtn9 deinococcus
39	1205.5	48.9	444	2 Q64Q81	Q64q81 bacteroides
40	1205.5	48.9	464	2 Q7WEU7	Q7weu7 bordetella
41	1202	48.8	448	2 Q88XM9	Q88xm9 lactobacill
42	1201	48.7	447	1 DHE4_ECOLI	P00370 escherichia
43	1200.5	48.7	446	2 Q6O9J6	Q6o9j6 trypanosoma
44	1200	48.7	449	2 Q6AJBI	Q6ajbi desulfotale
45	1199	48.6	443	2 Q97L29	Q97l29 clostridium

ALIGNMENTS

RESULT 1

ID	DHE4_CHLSO	STANDARD;	PRT;	523 AA.
AC	P28998;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	29-MAR-2004 (Rel. 43, Last annotation update)			
DE	NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)			
DE	(Fragment).			
OS	Chlorella sorokiniana.			
OC	Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;			
OC	Chlorellaceae; Chlorella.			
OX	NCBI_TaxID=3076;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92032762; PubMed=1718478;			
RA	Cook J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;			
RT	"A nuclear gene with many introns encoding ammonium-inducible			
RT	chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella			
RT	sorokiniana.";			
RL	Plant Mol. Biol. 17:1023-1044(1991).			
CC	-!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate			
CC	+ NH(3) + NADPH.			
CC	-!- SUBUNIT: Homo- and heterohexamers of alpha and beta subunits. Both			
CC	subunits are encoded by the same gene.			
CC	-!- SUBCELLULAR LOCATION: Chloroplast.			
CC	-!- INDUCTION: By ammonium.			
CC	-!- PTM: The N-termini of the alpha and the beta chains are blocked.			
CC	-!- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.			

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EMBL; X58832; CAA41636.1; --
EMBL; X58831; CAA41635.1; ALT_SEQ.
PIR; S17949; S17949.
HSSP; P24295; 1AUP.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV dehydrog_C.
InterPro; IPR006097; GLFV dehydrog_N.
Pfam; PF02028; GLFV dehydrog_1.
Pfam; PF02812; GLFV dehydrog_N; 1.
PRINTS; PR00082; GLFDHGNASE.
PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
Chloroplast; NADP; Oxidoreductase.
NON_TER 1
ACT SITE 202 202 By similarity.
SEQUENCE 523 AA; 57529 MW; A35FE730E5FEF974 CRC64;

Query Match 99.1%; Score 2444; DB 1; Length 523;
Best Local Similarity 99.2%; Pred. No. 1.7e-163;
Matches 472; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDATTGDFALQAVKQKATAGTGLVHGIKNPQVRLQLTIFPKDPEQBEFMAQVREV 60
DB 48 MDATTGDFALQAVKQKATAGTGLVHGIKNPBLQLTIFPKDPEQBEFMAQVREV 107

QY 61 AVSLOPVFEKRELLPIPKQIIVPEPVRITFRVSWLDDAGNLOVNRGFRVQYSSAIGPYKG 120
DB 108 AVSLOPVFEKRELLPIPKQIIVPEPVRITFRVSWLDDAGNLOVNRGFRVQYSSAIGPYKG 167

QY 121 GLRPHPSVNLSTMKFLAEPQIFKNSLTITLPMGGGKGGSDFDPKGSDAEVNRFCOSFMT 180
DB 168 GLRPHPSVNLSTMKFLAEPQIFKNSLTITLPMGGGKGGSDFDPKGSDAEVNRFCOSFMT 227

QY 181 LQRHISYVQDVPAGDIGVAREIGYLFQYKRITKNYTVGLTPKQEGGSEIRPEATGY 240
DB 228 LQRHISYVQDVPAGDIGVAREIGYLFQYKRITKNYTVGLTPKQEGGSEIRPEATGY 287

QY 241 GAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCAELLLEKGAIVLSDSQGYVYEPNG 300
DB 288 GAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCAELLLEKGAIVLSDSQGYVYEPNG 347

QY 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATONEIDEH 360
DB 348 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATONEIDEH 407

QY 361 DAELLIKHGCGQYVVEGANPSTNEAIHKYNKAGIICYPGKAANAGGVAVSGLEMTQNRMS 420
DB 408 DAELLIKHGCGQYVVEGANPSTNEAIHKYNKAGIICYPGKAANAGGVAVSGLEMTQNRMS 467

QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKQVADAVKAQAV 476
DB 468 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKQVADAVKAQAV 523

RESULT 2
Q8ILF7 PRELIMINARY; PRT; 510 AA.
AC Q8ILF7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase, putative.
GN ORFNames=PF1_0286;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angioli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.,
RT "Genome sequence of the human malaria parasite Plasmodium falciparum."
RL Nature 419:498-511(2002).
RL EMBL; AE014820; AAN36899.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF0208; GLFV_dehydrog; 1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.

DR PRINTS; PR00082; GLFDHGRGNASE
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
SQ SEQUENCE 510 AA; 5743 MW; AC400045297AC64P CRC64;

Query Match 55.8%; Score 1375; DB 2; Length 510;
Best Local Similarity 60.0%; Pred. No. 2.7e-88;
Matches 267; Conservative 66; Mismatches 104; Indels 8; Gaps 5;

QY 36 VRQLLTETPKDPSQBEFMAQVAVSLQVFPKRPBELLIFKQIVPEPVRITFRVSWL 95
DB 70 IEELREKVVSKNKEPEFLQAFEEVLSCLKPVFKDNVYIGVLENIAPERVIOPRVPMI 129

QY 96 DDAGNLQVNRFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAEPQIFKNSLTITLPMGGGK 155
DB 130 NDKEHKNRGRFRVQYNSVLGPYKGLRPHPSVNLSTMKFLAEPQIFKNSLTITLPMGGGK 189

QY 156 GGSDFDPKGSKDAEVMRFCQSFMTTELORHISYVQDVPAGDIGVAREIGYLFQYKRITK 215
DB 190 GGSDFDPKGSSEILLKFCQSFMTNLFRIYIGNTDVPAGDIGVAREIGYLFQYKLLKN 249

QY 216 NYTVGLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCA 275
DB 250 SFEGVLTKGNIKWGGNIRAEATGYGVYFAENVLKDNLNENKCKCLVSGSGNVAQYLV 309

QY 276 ELLLEKGAIVLSDSQGYVYEPNGFTREQLQAVQDMKKNNNSARISEY--KSDTAVYVG 333
DB 310 EKLTEKGAIVLUTMSDSNGYITLPENGFTREQLQAVQDMKKNNNSARISEY--KSDTAVYVG 367

QY 334 DRRKPWELDCQVDIAPPCATONEIDEHDAELLIKHGCGQYVVEGANPSTNEAIHKYNKAG 393
DB 368 ENQKPMNIPC--DIAPPCATONEINENDADLFQNKCKMIVEGANMPTHIKALHKLQNN 425

QY 394 ILYCPGKAANAGGVAVSGLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRY--N 451
DB 426 IILCPKAANAGGVAVSGLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRY--N 485

QY 452 VDLAAGANIAGFTKQVADAVKAQAV 476
DB 486 SDLVAGANIAGFLKVAADSFLQGG 510

RESULT 3
Q7RQ39 PRELIMINARY; PRT; 1203 AA.
AC Q7RQ39;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=PY01264;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angioli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.P., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.
RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC


```

Db 360 AGILYAPGKASAGGAVTSGLMSQNAIRLSWTREVDQRLFGIMQSHESCL-----KYG 415
QY 451 ----NVDLAAGANIAGFTKVAADAVKAQG 474
Db 416 KVGDTVNYVNGANIAGFVKVADAMLAQG 443

RESULT 9
Q9UT56
ID Q9UT56 PRELIMINARY; PRT; 444 AA.
AC DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase (EC 1.4.1.4).
GN Name=gdhA; OrderedLocusNames=NMA1964;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagals K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrett B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506 (2000).
DR EMBL; AL162757; CAB85184.1; -.
DR PIR; B81825; B81825.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016493; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02028; GLFV dehydrog. 1.
DR Pfam; PF02812; GLFV dehydrog. N; 1.
DR PRINTS; PR00082; GLFDHNRGNASE.
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 444 AA; 48462 MW; DE7F1A7B8DD6F424 CRC64;

Query Match 52.5%; Score 1294.5; DB 2; Length 444;
Best Local Similarity 57.1%; Pred. No. 1e-82;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 35 DVRLTLTEFMKDPPQOEPMQAVREVAVSLQVPEKRPPELL--PIPKQIVPERVITPRV 92
Db 3 DLNTLFLANLKQRNPQEPHQAVBEVFLSLDFLANPKYTOQSLELRIEVEPERVNRV 62

QY 93 SWLDAGNLQVNRGRFRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLLPMG 152
Db 63 TWQDDKGQVQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLLPMG 122

QY 153 GKGSDGDFPKGKSDAEVNRFCQSPMTLQRIHSYVQDVPAGDIGVAREIGYLFQGYKR 212
Db 123 GKGSDGDFPKGKSDAEVNRFCQSPMTLQRIHSYVQDVPAGDIGVAREIGYLFQGYKR 182

QY 213 ITKNTYTVLTPKQYGGSEIRPEATGYGAVLFEVNLKDGESLKGKCLVSGAGNVAQ 272
Db 183 INNEFSSVLTKGLFWGSLIRPEATGYGVVFAQNLQTRNDSFEGKRVLISGSGNVAQ 242

QY 273 YCAELLLKGAIVLSLSQGYVYBP-NGFTREQIQAQVDMKKNSARISYKSDTAVY 331
Db 243 YAAEKAIQIGAKVLTVSDSGVFLFPDSGMSQAALAEITELKEVRRE-RVATYAEQGLQ 301

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QY 332 VDGRKPHLDCQVDIAPPCATQNEIDHDABELLKHGCOYVVBGANPSTNEATHKYNK 391
Db 302 YFENQKPMGV--AAEIALPCATQNEIDHDABELLKHGCOYVVBGANPSTIGAVEQRIK 359

QY 392 AGIYCPGKAANAGGAVSGLSMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY- 450
Db 360 AGILYAPGKASAGGAVTSGLMSQNAIRLSWTREVDQRLFGIMQSHESCL-----KYG 415

QY 451 ----NVDLAAGANIAGFTKVAADAVKAQG 474
Db 416 KVGDTVNYVNGANIAGFVKVADAMLAQG 443

RESULT 10
Q88Q23
ID Q88Q23 PRELIMINARY; PRT; 449 AA.
AC DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=gdhA; OrderedLocusNames=PP0675;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160486;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzes A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eissen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AE016776; AAN66300.1; -.
DR HSP; P24295; 1AUP.
DR TIGR; PP0675; -.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02028; GLFV dehydrog. 1.
DR Pfam; PF02812; GLFV dehydrog. N; 1.
DR PRINTS; PR00082; GLFDHNRGNASE.
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 48871 MW; EF1733B6ABC89627 CRC64;

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Query Match 52.2%; Score 1287.5; DB 2; Length 449;
Best Local Similarity 58.2%; Pred. No. 3.3e-82;
Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4;

QY 36 VRLTLTEFMKDPPQOEPMQAVREVAVSLQVPEKRPPELL--IPKQIVPERVITPRVS 93
Db 8 VDNFLARLKQRDQPEPHQAVBEVRLTLPFLFANPHYLSGLERIVPERAVLFRVS 67

QY 94 WLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLLPMG 153
Db 68 WVDQKQVQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLLPMG 127

QY 154 GKGSDGDFPKGKSDAEVNRFCQSPMTLQRIHSYVQDVPAGDIGVAREIGYLFQGYKR 213
Db 128 GKGSDGDFPKGKSDAEVNRFCQSPMTLQRIHSYVQDVPAGDIGVAREIGYLFQGYKR 187

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QY 214 TKNYTGVLTTPKQOEYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQY 273
Db 188 ANQFTSVLTGKMTYGGSLRPEATGYGCVYFAEMLKRDKRIDRRVAVSGSGNVAQY 247
QY 274 CAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVG 333
Db 248 AARKVNDLGGKVISLSDSEGTLTAEAGLTDQWDMELKXVXR-GRISLACQFLEBFR 306
QY 334 DRKPKWELDCQVDIAFPCCATQNSIDEHDAELLIKHKGCQYVVEGANNPSTNEAIHKYNKAG 393
Db 307 KGQTPNSLPC--DIALPCATQNELGAEDARTLLRNGCICVAEGANNPTTLEAVDIFLDAG 364
QY 394 ILYCPKKAANAGGAVVSGLEMTQNRMSLNTWREVRDKLERIMKOIYDSAM--GPERRYN 451
Db 365 ILYAPKASNAGGAVVSGLEMSQNMRLNLTWAGEVDSKLHNMQSIHHACVHYGEADGR 424
QY 452 VDLAAGANTAGFTKVDADAKAQAQAV 476
Db 425 INYVKGANTAGFVKVADAMLAQGVV 449

RESULT 11
Q923C4
ID Q923C4 PRELIMINARY; PRT; 445 AA.
AC Q923C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NADP-glutamate dehydrogenase (EC 1.4.1.4).
GN Name=gdh;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAC1;
RA Ansari F.;
RL Thesis (1994), University of London London U.K.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PAC1, and PAO1;
RA Brown P.R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO1;
RA Ansari F.;
RL Thesis (1994), University of London, London U.K.
DR EMBL; Y18494; CAA77192.1; -.
DR EMBL; Y15166; CAA75437.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0014494; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006095; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006097; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02028; GLFV dehydrog. 1.
DR Pfam; PF02812; GLFV dehydrog. N; 1.
DR PRINTS; PR00082; GLFV dehydrog. N.
DR PROSITE; PS00074; GLFV dehydrog. N.
KW Oxidoreductase.
SQ SEQUENCE 445 AA; 48532 MW; B00DDE8E03A06D8A CRC64;

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Query Match 52.1%; Score 1285; DB 2; Length 445;
Best Local Similarity 58.4%; Pred. No. 4.8e-82;
Matches 261; Conservative 56; Mismatches 118; Indels 12; Gaps 5;
QY 36 VQLLTFEIMKDEQOEQMAVREAVSLQVFEKREPELLP--IPKQIVEPERVITFRVS 93
Db 5 VDAFLERLKRDPDQPEFHQAVEVLRLSLWPFLEAPHYLEAGIIRIIVEPERAILFRVP 64

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QY 94 WLDDAGNTQVNRGFRVQYSSAIGPYKGLRPHSPVNLSTIMKFLAEQIFKNSLTTLPMGG 153
Db 65 WYDDQGRVRVNRGFRVQYSSAIGPYKGLRPHSPVNLSTIMKFLAEQIFKNSLTTLPMGG 124
QY 154 KGKGSDFDPKGSDAEVMRFQCSFMTLORHLSYVQDVPAGDIGVGAREIGYLFQGYKRI 213
Db 125 KGKGSDFDPKGSDAEVMRFQCSFMTLORHLSYVQDVPAGDIGVGAREIGYLFQGYKRI 184
QY 214 TKNYTGVLTTPKQOEYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQY 273
Db 185 SNQFTSVLTGKLSYGGSLRPEATGYGCVYFAEMLKRDGRGFGDQORVAISGSGNVAQY 244
QY 274 CAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDT---AV 330
Db 245 AARKVMEMGGKVISLSDSEGTLTAEAGLSDQEWYLMELK---NARAGHPRDGVVFQFSL 300
QY 331 YVGRRKWELDCQVDIAFPCCATQNEIDEHDAELLIKHKGCQYVVEGANNPSTNEAIHKYN 390
Db 301 QFLEGVPPWGLAC--DIALPCATQNELDAEDARRLLANGCVCVAEGANNPSTLEAVDLFL 358
QY 391 KAGIYCPKKAANAGGAVVSGLEMTQNRMSLNTWREVRDKLERIMKOIYDSA-MGPSRR 449
Db 359 EAGIYAPKASNAGGAVVSGLEMSQNMRLNLTWAGEVDSKLHNMQSIHHACVHYGEADGR 424
QY 450 YNVDLAAGANTAGFTKVDADAKAQAQAV 476
Db 419 GRNVYKGANIAGFVKVADAMLAQGVV 445

RESULT 12
Q7YZU7
ID Q7YZU7 PRELIMINARY; PRT; 437 AA.
AC Q7YZU7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutamate dehydrogenase (Fragment).
GN Name=gdh;
OS Trichomonas vaginalis.
OC Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;
OC Trichomonadidae; Trichomonadinae; Trichomonas.
OX NCBI_TaxID=5722;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;
RA Andersson J.O., Roger A.J.;
RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene
transfer within and between prokaryotes and eukaryotes.";
RL BMC Evol. Biol. 3:14-14 (2003).
DR EMBL; AF533886; AAP83853.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02028; GLFV dehydrog. 1.
DR Pfam; PF02812; GLFV dehydrog. N; 1.
DR PROSITE; PS00074; GLFV dehydrog. N.
DR NON_TER 1
SQ SEQUENCE 437 AA; 47861 MW; 752055554DAFBFF96 CRC64;

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Query Match 52.1%; Score 1284.5; DB 2; Length 437;
Best Local Similarity 59.0%; Pred. No. 5.1e-82;
Matches 255; Conservative 56; Mismatches 118; Indels 3; Gaps 2;
QY 46 KDPEQEFMQAVREAVSLQVFEKREPELLPFIKQIVEPERVITFRVSWLDDAGNLQVNR 105
Db 4 RDPQKEFIQAVTEVLTSLVILEKEPKYQKLLPALVEPERVIMFRVFNVDKGMWNR 63
QY 106 GFRVQYSSAIGPYKGLRPHSPVNLSTIMKFLAEQIFKNSLTTLPMGGKGSDFDPKKG 165
Db 64 GFRVQYSSAIGPYKGLRPHSPVNLSTIMKFLAEQIFKNSLTTLPMGGKGSDFDPKKG 123

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QY 166 SDAEVMRFQCSFWTELORHISYVDVPAGDIGVGAREIGYLFQGYKRITKNYTVGLTPKG 225
DB 124 SGEVMRFQCSFWTELSRLSHTGNTDVPAGDIGVGAREIGYLFQGYKRITKNYTVGLTPKG 183
QY 226 QYGGSEIRPEATGAVGVFVENVLKDQGESLKGKRCVLSGAGNVAQYCAELLLKGAIV 285
DB 184 ISFGSLIRPEATGVLGVFTVTEMLRAGEEIKGRAMVSGNVAQYCCQKLMQLGAIP 243
QY 286 LSLSDSQYVYPNGFTREQLQAVQDMKK--KNSGARISEYKSDTAVY--VGDRRKPKWEL 342
DB 244 VSCSDSHGALIPKDGWTKHELDVNMHIKNVARTELKKISELPDLKGYEIDGKSIWACE 303
QY 343 CQVDTAFPCATONEIDEHDAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIYCPGKAA 402
DB 304 VPCDMGLPCATQNEILPEHPVIMVNGVKVLLAEGANMPSTNETIELYMKENIYYGPGKAA 363
QY 403 NAGGVAVSGLEWTONRMSLNWTRREVRDKLERIMKDIYDSAMGPRRRYVNDLAAGANTAG 462
DB 364 NAGGVAVSGLEWTONRMSLVRLANSEKVDKLEIMNIFEAHSAHQVGVPLYKGANLAG 423
QY 463 FTKVADAVKAQG 474
DB 424 FKRVADAMLAYG 435

RESULT 13
O96940 PRELIMINARY; PRT; 470 AA.
AC O96940;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
GN Names:GLUDH; Synonyms=GDH;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99089647; PubMed=9874251;
RA Wagner J.T., Luedemann H., Faerber P.M., Lottspeich F.,
RA Krauth-Siegel R.L.;
RT "Glutamate dehydrogenase, the marker protein of Plasmodium falciparum.
RT Cloning, expression and characterization of the malarial enzyme.";
RL Eur. J. Biochem. 258:813-819(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Li L.H., Li M., Wu Y.S., Wang P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12927; CAA73390.1; -.
DR EMBL; AY040586; AAK77969.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog_C.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF02028; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog_N; 1.
DR PRINTS; PR00082; GLFV dehydrog_N.
DR PROSITE; PS00074; GLFV dehydrog_N.
KW Oxidoreductase.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

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Query Match 51.9%; Score 1279.5; DB 2; Length 470;
Best Local Similarity 55.6%; Pred. No. 1.3e-81;
Matches 264; Conservative 62; Mismatches 130; Indels 19; Gaps 7;

QY 5 TGDFTALQKAVQMAKATKAGTEGVHGIKNPDRVQLLITEIFMKDPEQEQEVMQAVREVAVSL 64
DB 8 TGRFVVDK-----NASVYESIV-----DQEMNNVYRVKLPDPNQVEFLQAFHEILYSL 57

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QY 65 QPVFEKPELLPIKQIVPERVITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKGLRF 124
DB 58 KPLFMESPKYLPITETLSEPERAIQFRVCMDDNGVQRKNKCFRVQVNSALGPYKGLRF 117
QY 125 HPSVNLSTMKFLAPEQIFKNSLTTLPMCGGKGSGDFDPKGSDAEVMRFQCSFWTELRQH 184
DB 118 HPSVNLSTVKFLPEQIFKNSLTGLSMGGKGSGDFDPKGSDEILKFCQAFNNELYRH 177
QY 185 ISYVDVPAGDIGVGAREIGYLFQGYKRITKNYTVGLTPKGQYGGSEIRPEATGAVL 244
DB 178 IGPCTDVPAGDIGVGAREIGYLYGYKKIVNSFGTLTGKNVKGSGSNLRVEATGYGLVY 237
QY 245 FVENVLKDKGESLKGKRCVLSGAGNVAQYCAELLLKGAIVLSLSDSQYVVEGANMPSTRE 304
DB 238 FVLEVLKSLNTPVSKQTAVVSGGNVALYCVQKLLHNLNVKLTLSDSNGYVVEPNFGFTH 297
QY 305 QLOAVQDMKKKONNARSISEY--KSDTAVYVGDRAKPMELDCQVDIAFPACATONEIDEHDA 362
DB 298 NLEFLIDLKEE-KKGRIKEYLNHSTAKYF-PNEKPMGVPC--TLAFCATQNEINLEDA 353
QY 363 ELLIKHCQYVVEGANMPSTNEAIHKYNKAGIYCPGKAAAGVAVSGLEWTONRMSLN 422
DB 354 KLLQKNGCILVGEAGANMPSTVDALNPKSNNIYCPSKAANAGGVAISGLEMSQNFQPSH 413
QY 423 WTRREVRDKLERIMKDIYDSAMGPRRRY--NVDLAAGANTAGFTKVADAVKAQG 474
DB 414 WTRETVDEKLKEIMRNIPFIACSENALYTKNKYDLQAGANTAGFLUKVAESYIEQG 468

RESULT 14
Q8ILTO PRELIMINARY; PRT; 470 AA.
AC Q8ILTO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADP-specific glutamate dehydrogenase.
OS ORFNames=PF14_0164;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AB014818; AAN36776.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog_C.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF02028; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog_N; 1.
DR PRINTS; PR00082; GLFV dehydrog_N.
DR PROSITE; PS00074; GLFV dehydrog_N.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

Query Match 51.9%; Score 1279.5; DB 2; Length 470;
Best Local Similarity 55.6%; Pred. No. 1.3e-81;
Matches 264; Conservative 62; Mismatches 130; Indels 19; Gaps 7;

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```
QY 5 TGDFTALQKAVKQMATKAGTEGLVHGINKPNDVRQLLTELIPMKDPEQOEPMQAVREAVSL 64
Db 8 TGRFVVLDK-----NASVYESLV-----DQEMNNVYERVMKLDPNQVFLQAFHEILYSL 57
QY 65 QPVFEKRPELLPTFKOIVPERVITPRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPF 124
Db 58 KLFMEEPKYLPIETLSPEPAIQFRVCWLDGNGVQRKNRCFRVQYNSALGPYKGLRPF 117
QY 125 HPSVNLISIMKFLAFEQIFKNSLTTLPMGGKGGSDPDPKGSDAEVMRFQCSFMTLQRH 184
Db 118 HPSVNLISIVKFLGFEQIFKNSLTGLSMGGKGGSDPDPKGSNDNEILKFCQAFMNELYRH 177
QY 185 ISYVDVPAGDVGAGREIGYLFQYKRTIKYVTGVLTPKGOBYGGSEIRPEATGYGAVL 244
Db 178 IGPCTDVPAGDVGAGREIGYLYGQYKTVNSFNGTLTKNVKMGGSNLRVATGYGLVY 237
QY 245 FVENVLKDGESLKGKRCILVSGAGNVAQYCAELLEKGAIVLSLSDSQYVVEPNPGFTRE 304
Db 238 FVLEVLKSLNIPVEKQTAVVSGSNVALYCVQKLLHLNVKVLTLSDSNGYVVEPNPGFTHE 297
QY 305 QLVQVQDMKKKNSARISEY--KSDTAVYVGDGRRKPEWELDCQVDIAFPFCATQNEIDEHDA 362
Db 298 NLEFLIDLKEE-KKGRIKEYLNHSSSTAKYF-PNEKPGWGPC--TLAAPPFCATQNEINLEDA 353
QY 363 ELLIKHGCOYVVEGANMPTNBAIHKYKAGIYICPGKAANAGGVAVSGLEMTQNRMSLN 422
Db 354 KLLQKNGCILVGEGANMPTVDALNLFKSNIIYCPSKAANAGGVAISGLEMSQNFQFSH 413
QY 423 WTREREVDKLERIMKDIYDSAMGPSRRY---NVDLAAGANIAGFTKVADAVKAQG 474
Db 414 WTRRETVDKLEIMRNIFIACSENALKYTKNKYDLQAGANIAGFLKVAESYIEQG 468
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RESULT 15

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Q9TXS8
ID Q9TXS8 PRELIMINARY; PRT; 442 AA.
AC Q9TXS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=GDH;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]_TaxID=5833;
RP SEQUENCE FROM N.A.
RC STRAIN=FCQ 27;
RA Yuan P., Stewart T.S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098675; AAD11789.1; -.
DR HSSP; P24295; IAUJ.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog_C.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF02028; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog N; 1.
DR PRINTS; PR00082; GLFV dehydrogase.
DR PROSITE; PS00074; GLFV dehydrogenase; 1.
SQ SEQUENCE 442 AA; 49432 MW; 9D3F8AA679CCB4CC CRC64;
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Query Match 51.3%; Score 1265; DB 2; Length 442;
Best Local Similarity 58.8%; Pred. No. 1.2e-80;
Matches 258; Conservative 57; Mismatches 114; Indels 10; Gaps 6;

QY 42 EIFMK-DPEQOEPMQAVREAVSLQPVFEKRPELLDIPKQIVEPVIIFRVSWLDDAGN 100
Db 6 ERMVKLDPNQVFLQAFHEILYSLKPLFMEEPKYLPIETLSPEPAIQFRVCWLDNGV 65
QY 101 LQVNRGRFRVQYSSAIGPYKGLRFPSPVNLISIMKFLAFEQIFKNSLTTLPMGGKGGSDP 160
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Db 66 QRKNRCFRVQYNSALGPYKGLRFPSPVNLISIVKFLGFEQIFKNSLTGLSMGGKGGSDP 125
QY 161 DPKGSDAEVNRFCOSFMTLQRHISYYQDVDPAGDIGVGAREIGYLFQYKRTIKYNTGV 220
Db 126 DPKGSDNEILKFCQAFMNELYRHILGPCTDVPAGDIGVGRQIGYLYGQYKIVNSFNGT 185
QY 221 LTPKGOBYGGSEIRPEATGYGAVLFEVNLKDKGESLKGKRCILVSGAGNVAQYCAELLE 280
Db 186 LTGKNVKGGSNLRVATGYGLVYFVLEVLKSLNIPVEKQTAVVSGSNVALYCVQKLLH 245
QY 281 KGAIIVLSLSDSQYVVEPNPGFTREQLQAVQDMKKKNSARISEY--KSDTAVYVGDGRRK 338
Db 246 LNVKVLTLSDSNGYVVEPNPGFTHELEFLIDLKEE-KKGRIKEYLNHSSSTAKYF-PNEK 303
QY 339 WELDCQVDIAFPFCATQNEIDEHDAELLIKHGCOYVVEGANMPTNBAIHKYKAGIYICP 398
Db 304 WGVPC--TLAAPPFCATQNEINLEDAKLRKNGCILVGEGANMPTVDALNLFKSNIIYCP 361
QY 399 GKAAAGGVAVSGLEMTQNRMSLNWTREREVDKLERIMKDIYDSAMGPSRRY---NVDLA 455
Db 362 SKAANAGGVAISGLEMSQNFQFSHWTRRETVDKLEIMRNIFIACSENALKYTKNKYDLQ 421
QY 456 AGANIAGFTKVADAVKAQG 474
Db 422 AGANIAGFLKVAESYIEQG 440
```

Search completed: September 8, 2005, 02:43:31
Job time : 87.1641 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 02:27:13 ; Search time 20.6536 Seconds
(without alignments)
2217.496 Million cell updates/sec

Title: US-10-627-886-26
Perfect score: 2465
Sequence: 1 MDATTGDTALQKAVKQMAT.....GANIAGFTKVDVAKQAGV 476
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2444	99.1	523	1 S17949	glutamate dehydrog
2	1324.5	53.7	449	1 A42489	glutamate dehydrog
3	1309	53.1	445	2 H83072	glutamate dehydrog
4	1300.5	52.8	444	2 H81050	glutamate dehydrog
5	1294.5	52.5	444	2 B81825	glutamate dehydrog
6	1238	50.2	449	2 A64053	glutamate dehydrog
7	1214.5	49.3	444	2 T10487	glutamate dehydrog
8	1214	49.2	448	2 D98019	glutamate dehydrog
9	1212	49.2	448	2 H95151	glutamate dehydrog
10	1210.5	49.1	458	2 E83912	NADP-specific glut
11	1205.5	48.9	424	2 E75362	glutamate dehydrog
12	1201	48.7	447	1 DEECEN	glutamate dehydrog
13	1199	48.6	443	2 F96990	NADP-specific glut
14	1198	48.6	447	2 C90337	NADP-specific glut
15	1198	48.6	447	2 G85785	NADP-specific glut
16	1189.5	48.3	458	2 A11503	NADP-specific glut
17	1185	48.1	447	2 S32227	glutamate dehydrog
18	1182	48.0	447	1 A33504	glutamate dehydrog
19	1181	47.9	447	2 AF0710	NADP-specific glut
20	1180.5	47.9	458	2 A11144	NADP-specific glut
21	1153	46.8	447	2 AE0483	glutamate dehydrog
22	1150	46.7	448	2 D64567	glutamate dehydrog
23	1143	46.4	450	2 S22403	glutamate dehydrog
24	1142.5	46.3	448	2 B95277	probable glutamate
25	1139	46.2	448	2 F71862	glutamate dehydrog
26	1133.5	46.0	446	2 S06938	glutamate dehydrog
27	1121.5	45.5	454	1 DENCEN	glutamate dehydrog
28	1115.5	45.3	459	1 S04904	glutamate dehydrog
29	1109	45.0	457	2 S63608	glutamate dehydrog

30	1092	44.3	451	2 T41492	probable glutamate
31	1067.5	43.3	459	2 S17907	glutamate dehydrog
32	1037.5	42.1	454	1 A25275	glutamate dehydrog
33	1022	41.5	457	2 S51960	glutamate dehydrog
34	994.5	40.3	624	2 B96556	hypothetical proce
35	579.5	23.5	416	2 T45284	glutamate dehydrog
36	576.5	23.4	416	2 G72305	glutamate dehydrog
37	552.5	22.4	421	2 F83852	glutamate dehydrog
38	551	22.4	424	2 A70055	glutamate dehydrog
39	545.5	22.1	426	2 G69933	glutamate dehydrog
40	544.5	22.1	414	2 G89862	NAD-specific gluta
41	536	21.7	372	2 G84220	glutamate dehydrog
42	530	21.5	420	2 D75176	glutamate dehydrog
43	529.5	21.5	430	2 F83989	glutamate dehydrog
44	527.5	21.4	420	2 F84142	glutamate dehydrog
45	527.5	21.4	421	2 B81079	glutamate dehydrog

ALIGNMENTS

RESULT 1

S17949
glutamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fragment)
N:Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C:Species: Chlorella sorokiniana
C>Date: 30-Jun-1992 #sequence revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: S17949; S17950; S19030
R:Cock, J.M.; Kim, K.D.; Miller, P.W.; Hutson, R.G.; Schmidt, R.R.
Plant Mol. Biol. 17, 1023-1044, 1991
A:Title: A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP
A:Reference number: S17949; MUID:92032762; PMID:1718478
A:Accession: S17949
A:Molecule type: DNA
A:Residues: 1-523 <COC>
A:Cross-references: UNIPROT:P28998; EMBL:X58831
A:Accession: S17950
A:Molecule type: mRNA
A:Residues: 1-523 <COC2>
A:Cross-references: EMBL:X58832; NID:g18272; PIDN:CAA41636.1; PID:g18273
R:Schmidt, R.R.
submitted to the EMBL Data Library, April 1991
A:Reference number: S19030
A:Accession: S19030
A:Molecule type: DNA
A:Residues: 1-219, 'LW', 222-523 <SCH>
A:Cross-references: EMBL:X58831
C:Genetics:
A:Genome: nuclear
A:Introns: 6/2; 29/1; 40/3; 56/3; 85/3; 127/3; 149/3; 175/1; 183/3; 211/1; 246/1; 272/2;
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
C:Keywords: Chloroplast; hexamer; NADP; oxidoreductase
F:202/Binding site: substrate (Lys) #status predicted
Query Match 99.1%; Score 2444; DB 1; Length 523;
Best Local Similarity 99.2%; Pred. No. 1.2e-174;
Matches 472; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMQAVREV 60
Db 48 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMQAVREV 107
QY 61 AVSLQPVFEKPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 108 AVSLQPVFEKPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 167
QY 121 GLRFHPSVNLISIMKFLAEEQIFKNSLTTLPMGGGGKGSDFDPKGSDAEWMRFCSFWTE 180
Db 168 GLRFHPSVNLISIMKFLAEEQIFKNSLTTLPMGGGGKGSDFDPKGSDAEWMRFCSFWTE 227
QY 181 LQRHSYVQDVPAGDIGVAREIGYLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGY 240
Db 228 LQRHSYVQDVPAGDIGVAREIGYLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGY 287

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QY 241 GAVLFVENVLKDKGSLKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300
Db 288 GAVLFVENVLKDKGSLKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 347
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKRWELDCQVDIAPPCATQNEIDBH 360
Db 348 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKRWELDCQVDIAPPCATQNEIDBH 407
QY 361 DAELLIKHGCQYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 420
Db 408 DAELLIKHGCQYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 467
QY 421 LNWTRREVDKLERIMKDIYDSAMGPPSRRYNDLAAGANIAGFTKVADAVKAQGV 476
Db 468 LNWTRREVDKLERIMKDIYDSAMGPPSRRYNDLAAGANIAGFTKVADAVKAQGV 523

RESULT 2
A42489
Glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Giardia lamblia
N:Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C:Species: Giardia lamblia
C>Date: 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A42489
R:Yee, J.; Dennis, P.P.
J. Biol. Chem. 267, 7539-7544, 1992
A:Title: Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene
A:Note: sequence extracted from NCBI backbone (NCBIN:94071, NCBI:94074)
A:Reference number: A42489; MUID:92218410; PMID:155991
A:Accession: A42489
A:Keywords: NADP; oxidoreductase
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:CROSS-references: UNIPROT:P28724; GB:M84604; NID:gl59108; PID:AAA29155.1; PID:gl59109
A:Title: sequence extracted from NCBI backbone (NCBIN:94071, NCBI:94074)
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
F:125/Binding site: substrate (Lys) #status predicted

Query Match 53.7%; Score 1324.5; DB 1; Length 449;
Best Local Similarity 58.2%; Pred. No. 4e-91;
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5;

QY 36 VRQLLEIPMKDPEQOEPMQAVREAVASLQPVFEKRPPELLP--IFKQIVPEPVRTTPRSWL 95
Db 6 IELAVIKQRDHTEFQAEEVVDLSKVIFEREKPIPIPERKLEPERVILIFRPVPM 65
QY 96 DDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGK 155
Db 66 DDAGRLNVNRGRFRVQYSSALGPYKGLRPHPSVNLISILKFLGFEQILKNSLTTLPMGGGK 125
QY 156 GGSDFDPKGSDAEVMRFQCSFWTELQRIHSYVDVPAGDIGVAREIGYLPQYKRI 215
Db 126 GGSDFDPKGSDEVMRFQCSFWTELQRIHSYVDVPAGDIGVAREIGYLPQYKRLRN 185
QY 216 NVTGVLTPKQGVGSEIRPEATGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCA 275
Db 186 EFTGVLTKNVKGGSFIRPEATGAVLFVLEEMCKDNTVIRGNLLVSGSGNVAQFAC 245
QY 276 ELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKS---DTAVV 332
Db 246 EKLIQGAIVLTFSDNGTIVDKGFNEBKLAHLMLKNEKR-GRVSEFKDKYPSVAYYE 304
QY 333 GDRRKWE-LDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSNEAIHKYNK 391
Db 305 G--KKPWEFCQEQMPCATQNEVSGDDATRLVGLGLKFLVAEGANMPSNEAIVHVVHA 362
QY 392 AGIIVCPGAANAGGAVVSGLEMTQNRMSLNWTRREVDKLERIMKDIYDSAMGPPSRRYN 451
Db 363 KGVWGPAPKASNAGGAVVSGLEMSQNSVRLQWTAEEVDQKLRIMRGIFVACRDTAKYIG 422
QY 452 --VDLAAGANIAGFTKVADAVKAQGV 476
Db 423 HPKNYQMGANIAGFLKLVADSMIEQGCV 449
```

RESULT 3
H83072

glutamate dehydrogenase PA4588 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83072
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <STO>
A:CROSS-references: UNIPROT:Q9HVJ7; GB:AE004872; GB:AE004091; NID:g9950829; PID:AA0797
A:Experimental source: strain PA01
C:Genetics:
C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 53.1%; Score 1309; DB 2; Length 445;
Best Local Similarity 59.2%; Pred. No. 5.7e-90;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

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QY 36 VRQLLEIPMKDPEQOEPMQAVREAVASLQPVFEKRPPELLP--IFKQIVPEPVRTTPRSV 93
Db 5 VDAFLERLKRDDPDQPEHQAVVEVLSLWFLFLEAPHYLEAGIIEIVEPERAILFRVP 64
QY 94 WLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGG 153
Db 65 WVDDQGRVVRNVRGVRVQMSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGG 124
QY 154 GKGSDPDKGKSDAEVMRFQCSFWTELQRIHSYVDVPAGDIGVAREIGYLPQYKRI 213
Db 125 GKGSDPDKGKSDAEVMRFQCSFWTELQRIHSYVDVPAGDIGVAREIGYLPQYKRL 184
QY 214 TKNYTVLTPKQGVGSEIRPEATGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 273
Db 185 SNQTSVLTGKLSYSGSLIRPEATGCGVFAQEMLKDRGDPGQGVAVISGSGNVAQY 244
QY 274 CAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVVYG 333
Db 245 AARKVMEGKGVISLSDSEGTLYABAGLSDBQWEYLMELKNVRR-GRIREMAEQFSLQFL 303
QY 334 DRRKPEWELDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSNEAIHKYNKAG 393
Db 304 EGRRPWGLAC--DIALPCATQNEIDEHDAELLIKHGCQYVVEGANMPSNEAIHKYNKAG 361
QY 394 IIVCPGAANAGGAVVSGLEMTQNRMSLNWTRREVDKLERIMKDIYDSA-MGPSRRRYN 452
Db 362 ILVAPGKASNAGGAVVSGLEMSQNSAMRLRWSEGEVDYTKLHGIMQSIHACILLYGEEQGV 421
QY 453 DLAAAGANIAGFTKVADAVKAQGV 476
Db 422 NVYKGANIAGFKVADAMLAQGV 445
```

RESULT 4
H81050

glutamate dehydrogenase, NADP-specific NMB1710 [imported] - Neisseria meningitidis (strain 1809-1815)
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81050
R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain NC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: H81050

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-444 <TET>

A:Cross-references: UNIPROT:Q9JY71; GB:AE002521; GB:AE002098; NID:g7226962; PIDN:AAF4208

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1710

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 52.8%; Score 1300.5; DB 2; Length 444;

Best Local Similarity 57.4%; Pred. No. 2.4e-89;

Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 35 DVRLQLTEIFMKDPEQEFMQAVREAVSLQPVFEKRPPELL--PIFKQIVEPERVITFRV 92

DB 3 DLNLTFLPANLKQRPNQEPFHQAVEEVFMSLDPLAKNPKYTQOSLLERIVEPERVVMFRV 62

QY 93 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGGRLRPHSPVNLISIMKFLAEPQIFKNSLTTLPMG 152

DB 63 TWQDDKGQVQVNRGRVQYSSAIGPYKGGRLRPHSPVNLISIMKFLAEPQIFKNSLTTLPMG 122

QY 153 GKGGSDFDPKGSDAEVMRFQCSFMTELORHISYVQDVPAGDIGVGAREIGVLFQYK 212

DB 123 GKGGSDFDPKGSDAEVMRFQCSFMTELORHISYVQDVPAGDIGVGAREIGVLFQYK 182

QY 213 ITKNYTVGLTPKQEGYGGSEIRPEATGYGAVLFEVNLKDKGSLKGRCLVSGAGNVAQ 272

DB 183 IRNEFSVLTGKLEWGGSLIRPEATGYGCVVFAQAMLQTRNDSPEGKRVLSGSGNVAQ 242

QY 273 YCAELLEKGAVILSLDSQGYVYEP-NGFTREQLQAVQDMKKNSARISEKSTAVY 331

DB 243 YAAEKAIQLGAKVLTVDSDNGFVLPDPSGMSEAQLAALTELKEVRRE-RVATYAKEQGLQ 301

QY 332 VGDRRKPWELDCQVDIAPFCATQNEIDEHDAELLIKHGCQYVVEGANMPESTNEAIIHKYNK 391

DB 302 YFEKQKPGV--AAEIALPCATQNELDEEAAKTLANGCYVVAEGANMPESTLGAVEQFTK 359

QY 392 AGIIPCPCGAANAGGVAVSGLEMTQNRMSLNWTRBVRDKLERIMKDIYDSAMGPSRRY- 450

DB 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRBVRDQRLFGIMQSIHESCL----KYG 415

QY 451 ----NVDLAAGANIAGFTKVDADVAQAQ 474

DB 416 KVGDTVNVYNGANIAGFVKVADAMLAQ 443

QY 332 VGDRRKPWELDCQVDIAPFCATQNEIDEHDAELLIKHGCQYVVEGANMPESTNEAIIHKYNK 391

DB 302 YFEKQKPGV--AAEIALPCATQNELDEEAAKTLANGCYVVAEGANMPESTLGAVEQFTK 359

QY 392 AGIIPCPCGAANAGGVAVSGLEMTQNRMSLNWTRBVRDKLERIMKDIYDSAMGPSRRY- 450

DB 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRBVRDQRLFGIMQSIHESCL----KYG 415

QY 451 ----NVDLAAGANIAGFTKVDADVAQAQ 474

DB 416 KVGDTVNVYNGANIAGFVKVADAMLAQ 443

RESULT 5

B81825

Glutamate dehydrogenase (NADP) (EC 1.4.1.4) NMA1964 [imported] - Neisseria meningitidis

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: B81825

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jørgensen, K.; Leather, S.; Mølle, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: B81825

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-444 <PAR>

A:Cross-references: UNIPROT:Q8JTS6; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB8518

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: gdhA; NMA1964

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

C:Keywords: oxidoreductase

Query Match 52.5%; Score 1294.5; DB 2; Length 444;

Best Local Similarity 57.1%; Pred. No. 6.8e-89;

Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 35 DVRLQLTEIFMKDPEQEFMQAVREAVSLQPVFEKRPPELL--PIFKQIVEPERVITFRV 92

DB 3 DLNLTFLPANLKQRPNQEPFHQAVEEVFMSLDPLAKNPKYTQOSLLERIVEPERVVMFRV 62

QY 93 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGGRLRPHSPVNLISIMKFLAEPQIFKNSLTTLPMG 152

DB 63 TWQDDKGQVQVNRGRVQYSSAIGPYKGGRLRPHSPVNLISIMKFLAEPQIFKNSLTTLPMG 122

QY 153 GKGGSDFDPKGSDAEVMRFQCSFMTELORHISYVQDVPAGDIGVGAREIGVLFQYK 212

DB 123 GKGGSDFDPKGSDAEVMRFQCSFMTELORHISYVQDVPAGDIGVGAREIGVLFQYK 182

QY 213 ITKNYTVGLTPKQEGYGGSEIRPEATGYGAVLFEVNLKDKGSLKGRCLVSGAGNVAQ 272

DB 183 IRNEFSVLTGKLEWGGSLIRPEATGYGCVVFAQAMLQTRNDSPEGKRVLSGSGNVAQ 242

QY 273 YCAELLEKGAVILSLDSQGYVYEP-NGFTREQLQAVQDMKKNSARISEKSTAVY 331

DB 243 YAAEKAIQLGAKVLTVDSDNGFVLPDPSGMSEAQLAALTELKEVRRE-RVATYAKEQGLQ 301

QY 332 VGDRRKPWELDCQVDIAPFCATQNEIDEHDAELLIKHGCQYVVEGANMPESTNEAIIHKYNK 391

DB 302 YFEKQKPGV--AAEIALPCATQNELDEEAAKTLANGCYVVAEGANMPESTLGAVEQFTK 359

QY 392 AGIIPCPCGAANAGGVAVSGLEMTQNRMSLNWTRBVRDKLERIMKDIYDSAMGPSRRY- 450

DB 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRBVRDQRLFGIMQSIHESCL----KYG 415

QY 451 ----NVDLAAGANIAGFTKVDADVAQAQ 474

DB 416 KVGDTVNVYNGANIAGFVKVADAMLAQ 443

RESULT 6

A64053

glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C:Accession: A64053

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, S.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: A64053

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-449 <TIGR>

A:Cross-references: UNIPROT:P43793; GB:U32704; GB:L42023; NID:g1573143; PIDN:AAC21858.1.

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

C:Keywords: NADP; oxidoreductase

Query Match 50.2%; Score 1238; DB 2; Length 449;

Best Local Similarity 55.6%; Pred. No. 1.2e-84;

Matches 247; Conservative 64; Mismatches 111; Indels 16; Gaps 5;

QY 40 LTFIFMKDPEQEFMQAVREAVSLQPVFEKRPPELL--PIFKQIVEPERVITFRVSWLDD 97

DB 11 LTKVAQRDGYQPEFLQAVREVFTSWPFLANPKYRSEALLERLVEPERAFQFRVATDD 70

QY 98 AGNLQVNRGRFRVQYSSAIGPYKGGRLRPHSPVNLISIMKFLAEPQIFKNSLTTLPMGKGKG 157

DB 71 KGQVQVNRGRFRVQYSSAIGPYKGGRLRPHSPVNLISIMKFLAEPQIFKNSLTTLPMGKGKG 130

QY 158 SDFDPKGSDAEVMRFQCSFMTELORHISYVQDVPAGDIGVGAREIGVLFQYKRTKNY 217

DB 131 SDFDPKGSDAEVMRFQCSFMTELORHISYVQDVPAGDIGVGAREIGVLFQYKRTKNY 190

QY 218 TGVLTPKQEGYGGSEIRPEATGYGAVLFEVNLKDKGSLKGRCLVSGAGNVAQYCAEL 277

Db 191 ACVFTGRLSPGSLIRPEATGYGLIYFAQAMLAEGKDSFAGKVSVSGSNVAQYAIK 250
QY 278 LLEKGAIVLSLSDSQYVYEPNGFTREBQAOVDMKKGNNSARISEYKSDTAVYVGDRRK 337
Db 251 ALSLAGKVVTCSDSSGYVDPNGFTTEKLAALFDI-KNTKRGKVDYABQFGLQYFEGKR 309
QY 338 PHELDQVDDIAPFCATQNEIDEHDAELLIKHCQYVVEGANPSTNEAIHKYNKAGIYC 397
Db 310 PHEV--QVDIALPFCATQNEISLSDAQRLLKNGVKLVAGANPPTTEATEALLAADVLFG 367
QY 398 PKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDGSAMGPSRRY----- 450
Db 368 PKAANAGGAVVSGLEMAQSSQLYWTAAEVDQAQLHRIMLDIHANC-----KKYGTIEQOE 423
QY 451 NVDLAAGANIAGFTKVADAVKAQ 474
Db 424 NINYVVGANVAGFVKVADAMLAQ 447

RESULT 7
T10487
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola
C:Species: Prevotella ruminicola
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10487
R:Wen, Z.T.; Morrison, M.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z17049
A:Accession: T10487
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-444 <WEN>
A:Cross-references: UNIPROT:P95544; EMBL:U82240; NID:g1772844; PID:g1772845
A:Experimental source: strain B14
C:Genetics:
A:Note: gdhA
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
C:Keywords: NADP; oxidoreductase

Query Match 49.3%; Score 1214.5; DB 2; Length 444;
Best Local Similarity 54.9%; Pred. No. 6.5e-83;
Matches 242; Conservative 73; Mismatches 119; Indels 7; Gaps 4;

QY 38 QLLTEIFMKDPQOEPMQAVREAVLSQVPEKRPDL--LPFKQIVPERVITFRVSWL 95
Db 5 EVIEKLKAKFPQGPBYIQAVSQVLGTIEEYKNKHPFEKANLIERLCVDRILQFRVSW 64
QY 96 DDAGNLQVNRGPRVOYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLPWGGK 155
Db 65 DNGNVQTNLGRVQNNNAIGPYKGLRPHKSNVNSILKFLAPEQTFFKNSLTLPWGGAK 124
QY 156 GGSDFDPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRITK 215
Db 125 GGSDFDPHGSDEVMRFQCFPMNELYRLIGPDEDVPAGDIGVGREGVYMGFYKLLTH 184
QY 216 NYTGVLTTPKQYGGSEIRPEATGCAVLFEVNLKDGESLKGKRLVSGAGNVAQYCA 275
Db 185 PQGILTGKLEFGGSLIRPEATGYNVFLFEDMLKTRGESLEGKTLVSGSGNVAQYTI 244
QY 276 ELLLEKGAIVLSLSDSQYVYEPNGFTREBQAOVDMKKGNNSARISEYKSDTAVVGD 335
Db 245 EKLQLGAKPVTCSDSNGYIYDPGIDAELKAFIMELKNVRR-GRKEAYEKYGVYEN 303
QY 336 RXPWELDCQVDIAFPATQNEIDEHDAELLIKHCQYVVEGANPSTNEAIHKYNKAGII 395
Db 304 ARPW--GEKADIATPCATQDEINEABAKTLIANGVPAVSEGANPMTPEAAIKVFODAKIL 361
QY 396 YCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAM--GPSRRYND 453
Db 362 YCPGKASNAGGAVVATSGLEMSQNSRLSWTRREVDTKLNMIDHAIHNCVYKGTETPDGIN 421
QY 454 LAAGANIAGFTKVADAVKAQ 474

Db 422 YVKGANVAGFMKVAKAMMAQ 442

RESULT 8
D98019
glutamate dehydrogenase (NADP) (EC 1.4.1.4) [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: D98019
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Bargett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhten, S.; M
y, P.; Sun, P.M.; Winkler, M.E
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: D98019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-448 <KUR>
A:Cross-references: UNIPROT:Q8DPG0; GB:AE007317; PIDN:AAK99984.1; PID:g15458813; GSPDB:G
C:Genetics:
A:Gene: gdhA
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
C:Keywords: oxidoreductase

Query Match 49.2%; Score 1214; DB 2; Length 448;
Best Local Similarity 55.7%; Pred. No. 7.1e-83;
Matches 248; Conservative 62; Mismatches 127; Indels 8; Gaps 4;

QY 36 VRQLTEIFMKDPQOEPMQAVREAVLSQVPEKRPDL--LPFKQIVPERVITFRVSW 93
Db 8 IQSVFTVKARNGHEAEFLQAVBEFFNTLEVPFKHPHYEENILARITEPERVISFRVP 67
QY 94 WLDDAGNLQVNRGPRVOYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLPWGG 153
Db 68 WDRDGKQVNRGPRVQNSAVGPYKGLRPHPTVNOGILAPLGEQIFKNSLTLPWGG 127
QY 154 GKGSDFPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKR 213
Db 128 GKGSDFPKPKTDAEVMRFQCSFMTLQKHIGPSLDVPAGDIGVGREGIYLYQYKRL 187
QY 214 TKNYTVLTTPKQYGGSEIRPEATGCAVLFEVNLKDGESLKGKRLVSGAGNVAQY 273
Db 188 NQFDAGVLTGKPLGFGGSLIRPEATGYLVYTYTEMLKANGNSFAGKVVISGSGNVAQY 247
QY 274 CAELLEKGAIVLSLSDSQYVYEPNGFTREBQAOVDMKKGNNSARISEYKSDTAVVVG 333
Db 248 ALQKATELGATVIVSVDNSGVVIDENGI---DFDLLVDVKEKRR-ARLTETAAEKATATY 303
QY 334 DRRXPWELDCQVDIAFPATQNEIDEHDAELLIKHCQYVVEGANPSTNEAIHKYNKAG 393
Db 304 HEGSVTVAGNYDIALPCATQNEINGEAAKRLVAQGVICVSEGANMPSNLDAIKVYKENG 363
QY 394 ILYCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYV- 452
Db 364 IFYCPKAANAGGAVVSALEMSQNSRLSWTRREVDGRLKDIIMTNIFTAKTTSETYGLD 423
QY 453 -DLAAGANIAGFTKVADAVKAQ 476
Db 424 KDYLAGANIAFENVANMIAQ 448

RESULT 9
H95151
NADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae (strain TIGR
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95151
R:Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

QY 232 EIRPEATGYGAVLPVENVLKDKGESLKGKRCILVSGAGNVAQYCAELLLEKGAIVLSLSDS 291
 Db 181 LURPEATGYGVYFVEHMLRDQRMEMBLRVSVSGNVAQYAIKALHLGAHVLTASNS 240
 QY 292 QQYVYEPNGFTREQLQAVQDMKKKNSARISYKSDTAVVYDGRKRWELDCQVDIAPPC 351
 Db 241 GTVVDDEGFTYDKLAVLMDIKNER-GRVEDYAREVGAEPFGVRPW--DVPDVVALPC 297
 QY 352 ATONEIDEHDAELLKHGQYVVEGANMPSTNEAIIHKYNKAGIYCPCGAANAGGVAVSG 411
 Db 298 ATONELGADDARTLIAGGVVVAEGANPCDLAAIQAPPEAGVLYAPGKATNAGGVATSG 357
 QY 412 LEMTONRMSLNWTRREVRDKLERIMKDIYDSANGFSRR--YVVDLAAGANIAGFTKVADA 469
 Db 358 LEMSONAQRSLWTRREVRDQRLSIAHDSCLFYGRPRDRHVSVDLGDANTIAGFVKVATA 417
 QY 470 VKAQGA 476
 Db 418 MREQGV 424

RESULT 12
 DBECCN
 Glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Escherichia coli (strain K-12)
 N:Alternate names: glutamic dehydrogenase, NADP-specific glutamate dehydrogenase
 C:Species: Escherichia coli
 C:Date: 03-Aug-1984 #sequence revision 20-Sep-1984 #text_change 09-Jul-2004
 C:Accession: A00382; A22413; A64936
 R:McPherson, M.J.; Wootton, J.C.
 Nucleic Acids Res. 11, 5257-5266, 1983
 A:Title: Complete nucleotide sequence of the Escherichia coli gdhA gene.
 A:Reference number: A00382; MUID:83272967; PMID:6308576
 A:Accession: A00382
 A:Molecule type: DNA
 A:Residues: 1-447 <MCP>
 A:Cross-references: UNIPROT:P00370; GB:X00988; GB:J01615; GB:X00565; NID:G41543; PIDN:CA
 R:Valle, F.; Becerril, B.; Chen, E.; Seeburg, P.; Heyneker, H.; Bollivar, F.
 Gene 27, 193-199, 1984
 A:Title: Complete nucleotide sequence of the glutamate dehydrogenase gene from Escherich
 A:Reference number: A22413; MUID:84209849; PMID:6373501
 A:Accession: A22413
 A:Molecule type: DNA
 A:Residues: 1-447 <VAL>
 A:Experimental source: strain K12
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426817; PMID:9278503
 A:Accession: A64936
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-447 <BLAT>
 A:Cross-references: GB:AE000271; GB:U00096; NID:G1788058; PIDN:AAC74831.1; PID:G1788059;
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: gdhA
 A:Map position: 27 min
 A:Superfamily: glutamate dehydrogenase (NAD(P)+)
 C:Keywords: homohexamer; NADP; oxidoreductase
 F128/Binding site: substrate (Lys) #status predicted

Query Match 48.7%; Score 1201; DB 1; Length 447;
 Best Local Similarity 54.0%; Pred. No. 6.e-82;
 Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 36 VRLQLTETFMKDPQEQEFMQAVREAVVLSQPVFEKRPPELL--LPFKQIVPEPRTVTRVS 93
 Db 7 LESFLNHVQRPNQNTQTEFAQAVREVMVTLWPLFQNPQKYMQLERLSPERVVQFRVV 66
 QY 94 WDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAPEQIFKNSLTPLMG 153
 Db 67 WDDRNQIQVNRVQVSSAIGPYKGLRPHPSVNLSTMKFLAPEQIFKNSLTPLMG 126

QY 154 KGGSDFDPKCKSDAENVRFQCSFWTELQRHISYVQDVPAGDIGVGAREIGVLFQYKRI 213
 Db 127 KGGSDFDPKCKSEGVNRFQCALMTELYRLHGLADTDPAGDIGVGRGVGPMAGMMK 186
 QY 214 TKNYTVLTPKGOEYGGSEIRPEATGYGAVLPVENVLKDKGESLKGKRCILVSGAGNVAQY 273
 Db 187 SNNTACVFTPGKLGSGGLIRPEATGYGLVFTFAMLRKHQMGFGEMRVSVSGSNVAQY 246
 QY 274 CAELLLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISYKSDTAVVYDGRKRWELDCQVDIAPPC 351
 Db 247 ALEXAMEFGARVITASDSSGTVVDESFTKELARLIEI-KASRDGRVADYAKEGLVYL 305
 QY 334 DRRKRWELDCQVDIAPPCATONEIDEHDAELLKHGQYVVEGANMPSTNEAIIHKYNKAG 393
 Db 306 EGQFPWSL--PVDIALPCATQNELDVAHQIANGVKAVAEGANMPTTEATELFFQQAQ 363
 QY 394 ILYCPGKAANAGGVAVSGLEMTONRMSLNWTRREVRDKLERIMKDIYDSAM---CPSRRY 450
 Db 364 VLFAPGKAANAGGVATSGLEMAQNAARLGMKAEKVDARLHHIMLDIHHACEVHGEGEQ 423
 QY 451 NVDLAAGANIAGFTKVADAVKAQGA 476
 Db 424 N--YVQGANIAGFVKVADAMLAQGV 447

RESULT 13
 F96990
 NADP-specific glutamate dehydrogenase [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: F96990
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: F96990
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-443 <KUR>
 A:Cross-references: UNIPROT:Q97L29; GB:AE001437; PIDN:AAK78713.1; PID:G15023619; GSPDB:G
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC0737
 C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 48.6%; Score 1199; DB 2; Length 443;
 Best Local Similarity 54.4%; Pred. No. 9.2e-82;
 Matches 242; Conservative 69; Mismatches 122; Indels 12; Gaps 5;

QY 36 VRLQLTETFMKDPQEQEFMQAVREAVVLSQPVFEKRPPELL--LPFKQIVPEPRTVTRVS 93
 Db 4 LKHVMDVDVKNPNPNEPEFQAVKEVLSLEIVAEKHPWVKDKIPDKLIVERQIIFRVP 63
 QY 94 WDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAPEQIFKNSLTPLMG 153
 Db 64 WDDNGEBHINRPFRIQPNLSAIGPYKGLRPHPSVNLSTMKFLAPEQIFKNSLTPLMG 123
 QY 154 KGGSDFDPKCKSDAENVRFQCSFWTELQRHISYVQDVPAGDIGVGAREIGVLFQYKRI 213
 Db 124 KGGSDFPNPKSKNSSEIKRFQCSFMLELNKYIGANTDVPAGDIGVGRGVGPMAGMMK 183
 QY 214 TKNYTVLTPKGOEYGGSEIRPEATGYGAVLPVENVLKDKGESLKGKRCILVSGAGNVAQY 273
 Db 184 RNESGTVLTGKGLTGGSLVTEATGYGLCYPMNEALKAKGKSPDGAIVTISGSGNVAI 243
 QY 274 CAELLLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISYKSDTAVVYDGRKRWELDCQVDIAPPC 351
 Db 244 ANQKATQGAQVAMSDSNGIYDANGINLNTIRKIVEVERK---RIHEVTKYHPNASY 299
 QY 332 VGDREKRWELDCQVDIAPPCATONEIDEHDAELLKHGQYVVEGANMPSTNEAIIHKYNK 391

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:10:02 ; Search time 93.9092 Seconds
(without alignments)
1960.383 Million cell updates/sec

Title: US-10-627-886-26

Perfect score: 2465

Sequence: 1 MDATTGDTALQKAVKQMAT.....GANIAGFTKVADAVKQAGV 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003s:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2465	100.0	476	2	AAW15412 NADP-spec
2	2465	100.0	476	5	Aau98955 Mature NA
3	2465	100.0	476	8	Adq36731 Mature NA
4	2465	100.0	487	5	Aau98954 Mature NA
5	2465	100.0	487	8	Adq36729 Mature NA
6	2465	100.0	512	2	AAW15408 NADP-spec
7	2465	100.0	512	5	Aau98951 NADP-glut
8	2465	100.0	512	8	Adq36709 NADP-spec
9	2465	100.0	526	2	AAW15407 NADP-spec
10	2465	100.0	526	5	Aau98950 NADP-glut
11	2465	100.0	526	8	Adq36707 NADP-spec
12	2457	99.7	487	2	AAW15411 NADP-spec
13	1309	53.1	445	6	ABU38763 Protein e
14	1309	53.1	450	7	ABO71900 Pseudomon
15	1300.5	52.8	444	8	ADP08330 Neisseria
16	1297.5	52.6	444	6	ABP77942 N. gonorr
17	1297.5	52.6	444	6	ABU73205 Protein e
18	1294.5	52.5	444	5	Aau72986 Neisseria
19	1294.5	52.5	444	6	ABU38117 Protein e
20	1287.5	52.2	449	6	ABU39614 Protein e
21	1281	52.0	445	8	ADs24914 Bacterial
22	1259	51.1	454	8	ADN27186 Bacterial
23	1257.5	51.0	462	6	ABU17276 Protein e
24	1257.5	51.0	467	6	Ada34438 Acinetoba
25	1250.5	50.7	448	5	ABP65630 Bifidobac

26	1239.5	50.3	448	6	ABU29386 Protein e
27	1239.5	50.3	448	8	ADH97147 E. faecal
28	1239	50.3	449	5	Aau91467 Haemophil
29	1238	50.2	449	4	AAB88536 Haemophil
30	1238	50.2	449	6	ABU30172 Protein e
31	1236.5	50.2	449	5	ABP28423 Streptoco
32	1234.5	50.1	448	7	ADH85999 Enterococ
33	1230.5	49.9	449	6	ABU44405 Protein e
34	1230	49.9	449	8	ADK47974 Streptoco
35	1221	49.5	448	6	ADK47974 Streptoco
36	1214	49.2	448	6	ABU46100 Protein e
37	1212	49.2	448	6	ABU01740 S. pneumo
38	1211.5	49.1	448	8	ADH97149 E. faecal
39	1210.5	49.1	458	8	ADS28251 Bacterial
40	1207.5	49.0	464	6	ABU23354 Protein e
41	1205.5	48.9	424	8	ADN17964 Bacterial
42	1205.5	48.9	444	6	ABU20518 Protein e
43	1204	48.8	447	2	AAW08092 Glutamina
44	1201	48.7	447	2	AAW60830 E. coli g
45	1201	48.7	447	6	ABU15360 Protein e

ALIGNMENTS

RESULT 1

AAW15412

ID AAW15412 standard; protein; 476 AA.

AC AAW15412;

XX

XX

DT 17-OCT-2003 (revised)

DT 10-JUL-1997 (first entry)

XX

DE NADP-specific glutamate dehydrogenase beta subunit.

XX

KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;

KW chloroplast; transgenic plant.

XX

OS Chlorella sorokiniana; strain UTEX 1230.

XX

PN WO9712983-A1.

XX

PD 10-APR-1997.

XX

PF 03-OCT-1996; 96WO-US015921.

XX

PR 06-OCT-1995; 95US-00541033.

XX

XX (UYFL) UNIV FLORIDA.

PI Schmidt RR, Miller P;

XX

DR WPI; 1997-226226/20.

XX

XX N-PSDB; AAT64548.

PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella

XX sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism

PT plant cells.

XX

XX Claim 1; Page 48-50; 61pp; English.

XX

XX 2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature

CC alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an

CC ammonium-inducible, chloroplast-localised hexameric NADP-specific

CC glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.

CC They are produced by removal of transit peptides from the precursor

CC proteins (AAW15407-08). The N metabolism of plants can be modulated

CC (pref. increasing the assimilation of inorganic N into organic N) by

CC transforming them with nucleotide sequences (see also AAT64529-30,

CC AAT64547-48) encoding the alpha and/or beta subunits or precursor

CC proteins. Such plants show improved properties, e.g. increased crop yield

CC and improved stress tolerance. Heterohexamers having alpha and beta

CC subunits can be expressed that have higher aminating/deaminating activity
 CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 476 AA;

Query Match 100.0%; Score 2465; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3e-228;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIPMKDPEQEFMQAVREV 60
 DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIPMKDPEQEFMQAVREV 60

QY 61 AVSLQPVFEKRPPELLPIPKQIVPEPVRITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120
 DB 61 AVSLQPVFEKRPPELLPIPKQIVPEPVRITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120

QY 121 GLRPHPSVNLSTMKFLAEPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFQCSFMT 180
 DB 121 GLRPHPSVNLSTMKFLAEPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFQCSFMT 180

QY 181 LQRHISYVQDVPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGGSEIRPEATGY 240
 DB 181 LQRHISYVQDVPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGGSEIRPEATGY 240

QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
 DB 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVVVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360
 DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVVVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360

QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420
 DB 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420

QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476
 DB 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

RESULT 2

AAU98955
 ID AAU98955 standard; protein; 476 AA.

XX AAU98955;

XX 24-SEP-2002 (first entry)

XX Mature NADP-glutamate dehydrogenase beta subunit.

XX NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
 KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.

XX Chlorella sorokiniana.

XX US2002062495-A1.

XX 23-MAY-2002.

XX 01-MAY-1998; 98US-00070844.

XX 01-MAY-1998; 98US-00070844.

XX (SCHW/) SCHWIDT R R.

XX (MILL/) MILLER P.

XX Schmidt RR, Miller P;

XX WPI; 2002-499691/53.

DR N-PSDB; ABK51026.

XX Transforming a plant with a polynucleotide encoding a polypeptide with
 PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
 PT metabolism useful to increase yield and ammonium and osmotic stress
 PT tolerance.

XX Claim 7; Page 31-32; 35pp; English.

XX The invention relates to a method of modulating nitrogen metabolism in
 CC plant cells, comprising transforming a plant cell with a polynucleotide
 CC encoding a polypeptide having glutamate dehydrogenase activity, and
 CC culturing the cell to produce descendant cells which express the
 CC polypeptide. The method is used to provide plants with increased yield,
 CC improved ammonium assimilation properties, increased tolerance to ammonia
 CC toxicity, improved osmotic stress tolerance and improved composition. The
 CC present sequence represents the amino acid sequence of Chlorella
 CC sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the
 CC method of the invention

XX Sequence 476 AA;

Query Match 100.0%; Score 2465; DB 5; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3e-228;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIPMKDPEQEFMQAVREV 60

DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIPMKDPEQEFMQAVREV 60

QY 61 AVSLQPVFEKRPPELLPIPKQIVPEPVRITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120

DB 61 AVSLQPVFEKRPPELLPIPKQIVPEPVRITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120

QY 121 GLRPHPSVNLSTMKFLAEPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFQCSFMT 180

DB 121 GLRPHPSVNLSTMKFLAEPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFQCSFMT 180

QY 181 LQRHISYVQDVPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGGSEIRPEATGY 240

DB 181 LQRHISYVQDVPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGGSEIRPEATGY 240

QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300

DB 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVVVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360

DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVVVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360

QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420

DB 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420

QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

DB 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

RESULT 3

ADQ36731
 ID ADQ36731 standard; protein; 476 AA.

XX AC ADQ36731;

XX 23-SEP-2004 (first entry)

XX Mature NADP-specific GDH beta subunit, SEQ ID 26.

XX Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
 KW beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
 XX Chlorella sorokiniana.

QY 181 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKQGEYGGSEIRPEATGY 240
 Db 192 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKQGEYGGSEIRPEATGY 251
 QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300
 Db 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 311
 QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360
 Db 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 371
 QY 361 DAELLIKHGCGYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 420
 Db 372 DAELLIKHGCGYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 431
 QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476
 Db 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 487

RESULT 5

ADQ36729
 ID ADQ36729 standard; protein; 487 AA.
 XX ADQ36729;
 AC
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Mature NADP-specific GDH alpha subunit, SEQ ID 24.
 XX
 KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
 KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
 XX
 OS Chlorella sorokiniana.
 XX
 PN US2004128710-A1.
 XX
 PD 01-JUL-2004.
 XX
 PF 24-JUL-2003; 2003US-00627886.
 XX
 PR 01-MAY-1998; 98US-00070844.
 XX
 PA (SCHM/) SCHMIDT R R.
 PA (MILL/) MILLER P.
 XX
 PI Schmidt RR, Miller P;
 XX
 DR WPI; 2004-533134/51.
 DR N-PSDB; ADQ36728.
 XX

Increasing or decreasing nitrogen metabolism in plant cells, for plant
 PT with increased yield and improved tolerance to ammonia toxicity and
 PT osmotic stress, by transforming plant cell with nucleic acid having
 PT Glutamate dehydrogenase activity.
 XX
 PS Claim 7; SEQ ID NO 24; 36pp; English.
 XX
 CC The present invention relates to increasing or decreasing the nitrogen
 CC metabolism in plant cells by transforming a plant cell with a
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
 CC ADQ36731), or their fragments, which exhibit GDH activity. The
 CC polynucleotide is operably linked to a polynucleotide encoding a
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
 CC fragments that exhibit chloroplast transit activity. The method is useful
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The
 CC methods, polynucleotides, and polypeptides are useful in producing plant
 CC with increased yield, and with improved tolerance to ammonia toxicity,
 CC osmotic stress, and composition of the crop or plant. The present

CC sequence is the mature alpha subunit of the NADP-specific GDH used in the
 CC method of the invention.

XX Sequence 487 AA;

Query Match 100.0%; Score 2465; DB 8; Length 487;
 Best Local Similarity 100.0%; Pred. No. 3.1e-228;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDPVROLLEIFMKDPEQBEFMAQVREV 60
 Db 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDPVROLLEIFMKDPEQBEFMAQVREV 71

QY 61 AVSLQPVPEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
 Db 72 AVSLQPVPEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131

QY 121 GLRPHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFCSFWTE 180
 Db 132 GLRPHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFCSFWTE 191

QY 181 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKQGEYGGSEIRPEATGY 240
 Db 192 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKQGEYGGSEIRPEATGY 251

QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300
 Db 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 311

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360
 Db 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 371

QY 361 DAELLIKHGCGYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 420
 Db 372 DAELLIKHGCGYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 431

QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476
 Db 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 487

RESULT 6

AAW15408
 ID AAW15408 standard; protein; 512 AA.
 XX
 AC AAW15408;
 XX
 DT 17-OCT-2003 (revised)
 DT 10-JUL-1997 (first entry)
 XX
 DE NADP-specific glutamate dehydrogenase beta-subunit precursor.
 XX
 KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
 KW chloroplast; transgenic plant.
 XX
 OS Chlorella sorokiniana; strain UTEX 1230.
 XX
 PN WO9712983-A1.
 PN
 PD 10-APR-1997.
 XX
 PF 03-OCT-1996; 96WO-US015921.
 XX
 PR 06-OCT-1995; 95US-00541033.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Schmidt RR, Miller P;
 XX
 DR WPI; 1997-226226/20.
 DR N-PSDB; AAT64530, AAT64543.
 XX

PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PS plant cells.
XX
XX Claim 1; Page 29-32; 61pp; English.
XX
XX 2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha
CC (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-
CC inducible, chloroplast-localised NADP-specific glutamate dehydrogenase
CC (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha
CC and beta subunits (see also AAW15411-12) that comprise the active NADP-
CC GDH hexameric isoenzymes. The N metabolism of plants can be modulated
CC (pref. increasing the assimilation of inorganic N into organic N) by
CC transforming them with nucleotide sequences (see also AAT64529-30,
CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC proteins. Such plants show improved properties, e.g. increased crop yield
CC and improved stress tolerance. Heterohexamers having alpha and beta
CC subunits can be expressed that have higher aminating/deaminating activity
CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
CC (updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 512 AA;

Query Match 100.0%; Score 2465; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.4e-228;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQQBFMQAVREV 60
DB 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQQBFMQAVREV 96
QY 61 AVSLQPVFEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 97 AVSLQPVFEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFCSFMT 180
DB 157 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFCSFMT 216
QY 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKQEGYGSSEIRPEATGY 240
DB 217 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKQEGYGSSEIRPEATGY 276
QY 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQGYVPEP 300
DB 277 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQGYVPEP 336
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFPCCATQNEIDH 360
DB 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFPCCATQNEIDH 396
QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 420
DB 397 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 456
QY 421 LNWTRVEVRDKLERIMKDIYDSAMGPSRRYNYDLAAGANIAGFTKVADAVKAQGA 476
DB 457 LNWTRVEVRDKLERIMKDIYDSAMGPSRRYNYDLAAGANIAGFTKVADAVKAQGA 512

RESULT 7
AAU98951
ID AAU98951 standard; protein; 512 AA.
XX AAU98951;
AC
XX
DT 24-SEP-2002 (first entry)
XX NADP-glutamate dehydrogenase beta subunit.
XX NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.

XX Chlorella sorokiniana.
XX US2002062495-A1.
XX 23-MAY-2002.
XX
XX 01-MAY-1998; 98US-00070844.
XX 01-MAY-1998; 98US-00070844.
XX (SCHM/) SCHMIDT R R.
XX (MILL/) MILLER P.
XX Schmidt RR, Miller P;
XX WPI; 2002-499691/53.
XX N-PSDB; ABK51008.
XX
XX Transforming a plant with a polynucleotide encoding a polypeptide with
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
PT metabolism useful to increase yield and ammonium and osmotic stress
PT tolerance.
XX
XX Claim 6; Page 17-18; 35pp; English.
XX
XX The invention relates to a method of modulating nitrogen metabolism in
CC plant cells, comprising transforming a plant cell with a polynucleotide
CC encoding a polypeptide having glutamate dehydrogenase activity, and
CC culturing the cell to produce descendant cells which express the
CC polypeptide. The method is used to provide plants with increased yield,
CC improved ammonium assimilation properties, increased tolerance to ammonia
CC toxicity, improved osmotic stress tolerance and improved composition. The
CC present sequence represents the amino acid sequence of Chlorella
CC sorokiniana NADP-glutamate dehydrogenase beta subunit, used in the method
CC of the invention
XX
SQ Sequence 512 AA;

Query Match 100.0%; Score 2465; DB 5; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.4e-228;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQQBFMQAVREV 60
DB 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQQBFMQAVREV 96
QY 61 AVSLQPVFEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 97 AVSLQPVFEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFCSFMT 180
DB 157 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFCSFMT 216
QY 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKQEGYGSSEIRPEATGY 240
DB 217 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKQEGYGSSEIRPEATGY 276
QY 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQGYVPEP 300
DB 277 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQGYVPEP 336
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFPCCATQNEIDH 360
DB 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFPCCATQNEIDH 396
QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 420
DB 397 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 456
QY 421 LNWTRVEVRDKLERIMKDIYDSAMGPSRRYNYDLAAGANIAGFTKVADAVKAQGA 476
DB 457 LNWTRVEVRDKLERIMKDIYDSAMGPSRRYNYDLAAGANIAGFTKVADAVKAQGA 512

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Db 457 LNWTRREVRDKLERIMKDIYSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 512

RESULT 8
ID ADQ36709 standard; protein; 512 AA.
XX
AC ADQ36709;
XX
DT 23-SEP-2004 (first entry)
XX
DE NADP-specific GDH beta subunit precursor protein, SEQ ID 4.
XX
KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
KW beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
XX
OS Chlorella sorokiniana.
XX
PN US2004128710-A1.
XX
PD 01-JUL-2004.
XX
PF 24-JUL-2003; 2003US-00627886.
XX
PR 01-MAY-1998; 98US-00070844.
XX
PA (SCHM/) SCHMIDT R R.
PA (MILL/) MILLER P.
XX
PI Schmidt RR, Miller P;
XX
WPI, 2004-533134/51.
DR N-PSDB; ADQ36708.
XX
PT Increasing or decreasing nitrogen metabolism in plant cells, for plant
PT with increased yield and improved tolerance to ammonia toxicity and
PT osmotic stress, by transforming plant cell with nucleic acid having
PT glutamate dehydrogenase activity.
XX
PS Claim 7; SEQ ID NO 4; 36pp; English.
XX
CC The present invention relates to increasing or decreasing the nitrogen
CC metabolism in plant cells by transforming a plant cell with a
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
CC ADQ36731), or their fragments, which exhibits GDH activity. The
CC polynucleotide is operably linked to a polynucleotide encoding a
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
CC fragments that exhibit chloroplast transit activity. The method is useful
CC for increasing or decreasing the nitrogen metabolism in plant cells. The
CC methods, polynucleotides, and polypeptides are useful in producing plant
CC with increased yield, and with improved tolerance to ammonia toxicity,
CC osmotic stress, and composition of the crop or plant. The present
CC sequence is the precursor protein of the beta subunit of the NADP-
CC specific GDH, which is then processed to produce the mature alpha subunit
CC of the NADP-specific GDH, used in the method of the invention.
XX
SQ Sequence 512 AA;

Query Match 100.0%; Score 2465; DB 8; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.4e-228; Mismatches 0; Gaps 0;
Matches 476; Conservative 0; Indels 0;

QY 1 MDATTGDDFTALQKAVKQMATKAGTGLVHGINKNPVDRQLLTIFPMKDPQQEFMQAVREV 60
DB 37 MDATTGDDFTALQKAVKQMATKAGTGLVHGINKNPVDRQLLTIFPMKDPQQEFMQAVREV 96
QY 61 AVSLQPVFEKRPPELLPIPKQIIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 97 AVSLQPVFEKRPPELLPIPKQIIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRFHPSVNLISIMKFLAFEQIPKNSLTLPMSGGGKGSDFDPKGSDAEVMRFQSPWTE 180

Db 157 GLRFHPSVNLISIMKFLAFEQIPKNSLTLPMSGGGKGSDFDPKGSDAEVMRFQSPWTE 216
QY 181 LQRHISYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGQYGGSEIRPEATGY 240
DB 217 LQRHISYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGQYGGSEIRPEATGY 276
QY 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQYVYBPNG 300
DB 277 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQYVYBPNG 336
QY 301 FTRSQLQAVQDMKKKNSARISEYKSDTAVVVGDRRKPWELDCQVDIAFPCCATONEIDEH 360
DB 337 FTRSQLQAVQDMKKKNSARISEYKSDTAVVVGDRRKPWELDCQVDIAFPCCATONEIDEH 396
QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420
DB 397 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 456
QY 421 LNWTRREVRDKLERIMKDIYSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476
DB 457 LNWTRREVRDKLERIMKDIYSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 512

RESULT 9
AAW15407
ID AAW15407 standard; protein; 526 AA.
XX
AC AAW15407;
XX
DT 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
DE NADP-specific glutamate dehydrogenase alpha-subunit precursor.
XX
KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW chloroplast; transgenic plant.
XX
OS Chlorella sorokiniana; strain UTEX 1230.
XX
PN WO9712983-A1.
XX
PD 10-APR-1997.
XX
PF 03-OCT-1996; 96WO-US015921.
XX
PR 06-OCT-1995; 95US-00541033.
XX
PA (UYFL ) UNIV FLORIDA.
XX
PI Schmidt RR, Miller P;
XX
WPI, 1997-226226/20.
DR N-PSDB; AAT64529, AAT64542.
XX
CC DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
CC sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
CC plant cells.
XX
PS Claim 1; Page 25-27; 61pp; English.
XX
CC 2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha
CC (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-
CC inducible, chloroplast-localised NADP-specific glutamate dehydrogenase
CC (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha
CC and beta subunits (see also AAW15411-12) that comprise the active NADP-
CC GDH hexameric isoenzymes. The N metabolism of plants can be modulated
CC (pref. increasing the assimilation of inorganic N into organic N) by
CC transforming them with nucleotide sequences (see also AAT64529-30,
CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC proteins. Such plants show improved properties, e.g. increased crop yield
CC and improved stress tolerance. Heterohexamers having alpha and beta
CC subunits can be expressed that have higher aminating/deaminating activity
```


CC ratios (i.e. higher capacity for glutamate synthesis) than homoexamers.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 526 AA;

Query Match 100.0%; Score 2465; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 3.5e-228;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQBFMQAVREV 60
DB 51 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQBFMQAVREV 110

QY 61 AVSLQPVFEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 111 AVSLQPVFEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170

QY 121 GLRFHPSVNLSTMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEVWRFCSFMTE 180
DB 171 GLRFHPSVNLSTMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEVWRFCSFMTE 230

QY 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRTKNTYTGVLTPKGOEYGSSEIRPEATGY 240
DB 231 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRTKNTYTGVLTPKGOEYGSSEIRPEATGY 290

QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300
DB 291 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 350

QY 301 FTREOLQAVQDMKKKNSARISEYKSDTAVYVGDRLKPWELDCQVDIAFPCCATQNEIDEH 360
DB 351 FTREOLQAVQDMKKKNSARISEYKSDTAVYVGDRLKPWELDCQVDIAFPCCATQNEIDEH 410

QY 361 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
DB 411 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 470

QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 476
DB 471 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 526

RESULT 10
AAU98950
ID AAU98950 standard; protein; 526 AA.
AC AAU98950;
XX
DT 24-SEP-2002 (first entry)
XX
DE NADP-glutamate dehydrogenase alpha subunit.
XX
KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
XX
OS Chlorella sorokiniana.
XX
PN US2002062495-A1.
XX
PD 23-MAY-2002.
XX
PF 01-MAY-1998; 98US-00070844.
XX
PR 01-MAY-1998; 98US-00070844.
XX
PA (SCHM/) SCHMIDT R R.
PA (MILL/) MILLER P.
XX
PI Schmidt RR, Miller P;
XX WPI; 2002-499691/53.
XX N-PSDB; ABK51007.
DR

XX
PT Transforming a plant with a polynucleotide encoding a polypeptide with
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
PT metabolism useful to increase yield and ammonium and osmotic stress
PT tolerance.
XX
PS Claim 6; Page 13-15; 35pp; English.
XX
CC The invention relates to a method of modulating nitrogen metabolism in
CC plant cells, comprising transcribing a plant cell with a polynucleotide
CC encoding a polypeptide having glutamate dehydrogenase activity, and
CC culturing the cell to produce descendant cells which express the
CC polypeptide. The method is used to provide plants with increased yield,
CC improved ammonium assimilation properties, increased tolerance to ammonia
CC toxicity, improved osmotic stress tolerance and improved composition. The
CC present sequence represents the amino acid sequence of Chlorella
CC sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the
CC method of the invention
XX
SQ Sequence 526 AA;

Query Match 100.0%; Score 2465; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 3.5e-228;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQBFMQAVREV 60
DB 51 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQBFMQAVREV 110

QY 61 AVSLQPVFEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 111 AVSLQPVFEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170

QY 121 GLRFHPSVNLSTMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEVWRFCSFMTE 180
DB 171 GLRFHPSVNLSTMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEVWRFCSFMTE 230

QY 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRTKNTYTGVLTPKGOEYGSSEIRPEATGY 240
DB 231 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRTKNTYTGVLTPKGOEYGSSEIRPEATGY 290

QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300
DB 291 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 350

QY 301 FTREOLQAVQDMKKKNSARISEYKSDTAVYVGDRLKPWELDCQVDIAFPCCATQNEIDEH 360
DB 351 FTREOLQAVQDMKKKNSARISEYKSDTAVYVGDRLKPWELDCQVDIAFPCCATQNEIDEH 410

QY 361 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
DB 411 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 470

QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 476
DB 471 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 526

RESULT 11
ADQ36707
ID ADQ36707 standard; protein; 526 AA.
XX
AC ADQ36707;
XX
DT 23-SEP-2004 (first entry)
XX
DE NADP-specific GDH alpha subunit precursor protein, SEQ ID 2.
XX
KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
XX
OS Chlorella sorokiniana.
XX

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PN US2004128710-A1.
XX
PD
XX
XX 01-JUL-2004.
XX
XX 24-JUL-2003; 2003US-00627886.
XX
XX
PR 01-MAY-1998; 98US-00070844.
XX
XX (SCHM/) SCHMIDT R R.
PA (MILL/) MILLER P.
XX
XX Schmidt RR, Miller P;
PI
XX
XX WPI, 2004-533134/51.
DR N-PSDB; ADQ36706.
XX
XX Increasing or decreasing nitrogen metabolism in plant cells, for plant
PT with increased yield and improved tolerance to ammonia toxicity and
PT osmotic stress, by transforming plant cell with nucleic acid having
PT glutamate dehydrogenase activity.
XX
XX Claim 7; SEQ ID NO 2; 36pp; English.
PS
XX The present invention relates to increasing or decreasing the nitrogen
CC metabolism in plant cells by transforming a plant cell with a
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
CC ADQ36731), or their fragments, which exhibits GDH activity. The
CC polynucleotide is operably linked to a polynucleotide encoding a
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
CC fragments that exhibit chloroplast transit activity. The method is useful
CC for increasing or decreasing the nitrogen metabolism in plant cells. The
CC methods, polynucleotides, and polypeptides are useful in producing plant
CC with increased yield, and with improved tolerance to ammonia toxicity,
CC osmotic stress, and composition of the crop or plant. The present
CC sequence is the precursor protein of the alpha subunit of the NADP-
CC specific GDH, which is then processed to produce the mature alpha subunit
CC of the NADP-specific GDH, used in the method of the invention.
XX
XX Sequence 526 AA;
SQ
Query Match 100.0%; Score 2465; DB 8; Length 526;
Best Local Similarity 100.0%; Pred. No. 3.5e-228; Mismatches 0; Indels 0; Gaps 0;
Matches 476; Conservative 0;

QY 1 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPDVRLQLTEIFMKDPEQEFMQAVREV 60
Db 51 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPDVRLQLTEIFMKDPEQEFMQAVREV 110
QY 61 AVSLQPVPEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 111 AVSLQPVPEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
QY 121 GLRHPSVNLSTIMKFLAPEQIFKNSLTTLPMGGGKGSGDFDPKGSDAEVMRFQCSFTE 180
Db 171 GLRHPSVNLSTIMKFLAPEQIFKNSLTTLPMGGGKGSGDFDPKGSDAEVMRFQCSFTE 230
QY 181 LQRHISYVQDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGY 240
Db 231 LQRHISYVQDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGY 290
QY 241 GAVLFVENVLKDGSLKGRCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 300
Db 291 GAVLFVENVLKDGSLKGRCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 350
QY 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGDRRKPNWELDCQVDIAPPQATONEIDEH 360
Db 351 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGDRRKPNWELDCQVDIAPPQATONEIDEH 410
QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPCGAANAGGAVSGLGEMTQNRMS 420
Db 411 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPCGAANAGGAVSGLGEMTQNRMS 470

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QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDADVAKQGA 476
Db 471 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDADVAKQGA 526

RESULT 12
AAW15411
ID AAW15411 standard; protein; 487 AA.
XX
XX AAW15411;
XX
XX 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
XX NADP-specific glutamate dehydrogenase alpha subunit.
XX
XX Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW chloroplast; transgenic plant.
XX
XX Chlorella sorokiniana; strain UTEX 1230.
XX
XX WO9712983-A1.
XX
XX 10-APR-1997.
XX
XX 03-OCT-1996; 96WO-US015921.
XX
XX 06-OCT-1995; 95US-00541033.
XX
XX (UYFL ) UNIV FLORIDA.
XX
XX Schmidt RR, Miller P;
PI
XX WPI; 1997-226226/20.
DR N-PSDB; AAT64547.
XX
XX DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT plant cells.
PT
PS Claim 1; Page 44-46; 61pp; English.
XX
XX 2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature
CC alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an
CC ammonium-inducible, chloroplast-localised hexameric NADP-specific
CC glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
CC They are produced by removal of transit peptides from the precursor
CC proteins (AAW15407-08). The N metabolism of plants can be modulated
CC (pref. increasing the assimilation of inorganic N into organic N) by
CC transforming them with nucleotide sequences (see also AAT64529-30,
CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC proteins. Such plants show improved properties, e.g. increased crop yield
CC and improved stress tolerance. Heterohexamers having alpha and beta
CC subunits can be expressed that have higher aminating/deaminating activity
CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 487 AA;
SQ
Query Match 99.7%; Score 2457; DB 2; Length 487;
Best Local Similarity 99.8%; Pred. No. 1.8e-227;
Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPDVRLQLTEIFMKDPEQEFMQAVREV 60
Db 12 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPDVRLQLTEIFMKDPEQEFMQAVREV 71
QY 61 AVSLQPVPEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 72 AVSLQPVPEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
QY 121 GLRHPSVNLSTIMKFLAPEQIFKNSLTTLPMGGGKGSGDFDPKGSDAEVMRFQCSFTE 180

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Db 132 GURFHPSVNLIMKFLAFQIPKNSLTLPMGGKGGSDPDKGKSDAEVIMRFSOFMTE 191
QY 181 LQRHISYVQDVDPAGDIGVGAREIGYLFQGYKRTTKNYTGLTPKGOEYGGSEIRPEATCY 240
Db 192 LQRHISYVQDVDPAGDIGVGAREIGYLFQGYKRTTKNYTGLTPKGOEYGGSEIRPEATCY 251
QY 241 GAVLFVENVLKKGESLKGKRCILVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 300
Db 252 GAVLFVENVLKKGESLKGKRCILVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 311
QY 301 FTREQLQAVQDMKKKNSARISYKSDTAVYVGDGRKPMELDCVDIAPPCATONEIDRH 360
Db 312 FTREQLQAVQDMKKKNSARISYKSDTAVYVGDGRKPMELDCVDIAPPCATONEIDRH 371
QY 361 DAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 420
Db 372 DAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 431
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYNDLAAGANAGFTKVADAVKAQGV 476
Db 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYNDLAAGANAGFTKVADAVKAQGV 487

RESULT 13

ABU38763
ID ABU38763 standard; protein; 445 AA.

AC ABU38763;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #24290.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Pseudomonas aeruginosa.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA42633.

XX Claim 25; SEQ ID NO 66687; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 445 AA;

Query Match 53.1%; Score 1309; DB 6; Length 445;
Best Local Similarity 59.2%; Pred. No. 8.2e-117;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 36 VRLQTEIFMKDPEQOEPMQAVREVAVSLQVFEKRPBLLP--IPKQIVEPBRVITFRVS 93
Db 5 VDAFLERLKRDPDQDFEFHQAVVEVRLSPFPLEANPHYLEAGITIERIVEPERAILFRVP 64
QY 94 WLDDAGNLQVNRGRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTLPMGG 153
Db 65 WDDQGRVRVNRGVRQVMSAIGPYKGLRPHPSVNLGLKFLAFEQIFKNSLTLPMGG 124
QY 154 KGKGSDFDPKGSDAEVMRFQCSFMTELQRHISYVQDVDPAGDIGVGAREIGYLFQYKRI 213
Db 125 KGKGSDFDPKGSDAEVMRFQCSFMSELYRHVGADLDVPAGDIGVGAREIGYLFQYKRL 184
QY 214 TKNYTGVLTPKGOEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCILVSGAGNVAQY 273
Db 185 SNQFTSVLTGKLSYGGSLIRPEATGFCVYFAQEMLKDRGRGFDGQVRVAISGSGNVAQY 244
QY 274 CAELLLKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYV 333
Db 245 AARKVMEMGGKVISLSDEGTLYABAGLSDQWYLMELKNVRR-GRIREMAEQFSLOFL 303
QY 334 DRKPEWELDCQVDIAPPCATONEIDEHDAELLIKHCQYVVEGANMPSTNEAIHKYNKAG 393
Db 304 EGRRPWGLAC--DIALPCATQNELDAEDARRLLANGCVCAEGANMPSTLEAVDLFLEAG 361
QY 394 IYICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGPSRRYV 452
Db 362 ILYAPGKASNAGGAVVSGLEMSQNAMLRWSEGEVDTKLHGIMQSIHACLLIYGEQGRV 421
QY 453 DLAAGANAGFTKVADAVKAQGV 476
Db 422 NYVKGANAGFTKVADAVKAQGV 445

RESULT 14

ABO71900
ID ABO71900 standard; protein; 450 AA.

XX ABO71900;

XX 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #4075.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS *Pseudomonas aeruginosa*.
XX PN US551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX DR WPI; 2003-615309/58.
XX DR N-PSDB; ABD05471.
XX PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide, of
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX PS Disclosure; SEQ ID NO 20646; 455pp; English.
XX CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,
XX CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
XX CC effective antibacterial targets, as targets for antibacterial drugs,
XX CC including anti-*P. aeruginosa* drugs, as templates for recombinant
XX CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
XX CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
XX CC infection, and in detection of *P. aeruginosa* sequences or other sequences
XX CC of *Pseudomonas* species using biochip technology. Sequences ABO67826-
XX CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format from USPTO at
XX CC seqdata.uspto.gov/sequence.html
XX SQ Sequence 450 AA;

Query Match 53.1%; Score 1309; DB 7; Length 450;
Best Local Similarity 59.2%; Pred. No. 8.3e-117;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 36 VRLQLTEIFMKDPEQEFMQAVREAVSLQPVFEKPELLP--IFKQIVPERVITFRVS 93
DB 10 VDAFLERLKRDPDQDPFQAVVEVLRSLWPLFANPHYLEAGIITERIVEPERALFRVP 69
QY 94 WLDDAGNLQVNRGFRVQYSSAIGPYKGGIRPHSPVNLSTMKFLAPEQIFKNSLTLLPMGG 153
DB 70 WDDQGRVRNRYGVQVSSALGPYKGGIRPHSPVNLSTMKFLAPEQIFKNSLTLLPMGG 129
QY 154 KGSGSDFPDKGSDAEVNRFCQSPMSLYRHVGADLDVPAGDIGVGAREIGYLFQYKRI 213
DB 130 KGSGSDFPDKGSDAEVNRFCQSPMSLYRHVGADLDVPAGDIGVGAREIGYLFQYKRI 189
QY 214 TQNYTGVLTPKQEGGSEIRPCTGYGAVLVNVDKESLKGKCLVSGAGNVAQY 273
DB 190 SNQFTSVLTGKSLVGGSLIRPEATGFCVYPAQEMLKDRGRGDFGQVRVAISGNGVAQY 249
QY 274 CAELLEKGAIVLSLSDSGYVYVPENGFTREQLQAVQDMKKNGNARISEYKSDTAVVVG 333
DB 250 AARKVMWGGKVVISLSDSEGLYAEAGLSDQWEYIMELKNYR--GRITMAEQSLQFL 308
QY 334 DRKFWELDCQVDIAPPATONIEIDHDAELLIKHGCGQYVVEGANPSTNEAIHKYNKAG 393
DB 309 EGRREWGLAC--DIALPCATONELDAEDARRLLANGCVCAEGANNPSTLEAVDLFLEAG 366
QY 394 IYICPGKAANAGVAVSGLEMTQNRMSLNWTREVRDRLKLRIMKDIYDSA-MGPSRRYV 452

Db 367 ILVAPGRASNAGGVAVSGLEMSQAMRLRWSEGEVDTKLHGIMQSIHACILLYGEEQGRV 426
QY 453 DLAAAGANIAGFTKVADAVKAQGV 476
Db 427 NYVKGANIAGFPVKVADAMLAQGVV 450

RESULT 15
ADP08330
ID ADP08330 standard; protein; 444 AA.
XX AC ADP08330;
XX DT 26-AUG-2004 (first entry)
XX DE *Neisseria meningitidis* MCS8 OMV-related membrane protein - SEQ ID 163.
XX KW outer-membrane vesicle; antibacterial; antiinflammatory;
XX KW meningococcal protein trafficking; localisation; infection; vaccine;
XX KW gene therapy.
XX OS *Neisseria meningitidis* MCS8.
XX PN WO2004046177-A2.
XX PD 03-JUN-2004.
XX PF 17-NOV-2003; 2003WO-IB006281.
XX PR 15-NOV-2002; 2002GB-00026734.
XX PR 27-MAR-2003; 2003GB-00007131.
XX PA (CHIR) CHIRON SRL.
XX PI Norais N, Grandi G;
XX DR WPI; 2004-420615/39.
XX PT New compositions having outer-membrane vesicles and proteins from
XX PT *Neisseria meningitidis*, useful in the field of meningococcal
XX PT biochemistry, in particular for preventing and/or treating meningococcal
XX PT infections.
XX PS Claim 9; SEQ ID NO 163; 79pp; English.
XX CC The invention relates to a novel composition comprising outer-membrane
XX CC vesicles (OMV) prepared from a first strain of *Neisseria meningitidis* and
XX CC 1 or more proteins which are present in OMVs prepared from a second
XX CC strain of *N. meningitidis*, but which are not present in OMVs prepared
XX CC from the first strain. The composition of the invention demonstrates
XX CC antibacterial and antiinflammatory activities and may be useful in the
XX CC field of meningococcal biochemistry, in particular the trafficking and
XX CC localisation of meningococcal proteins, as well as in the prevention or
XX CC treatment of meningococcal infections, possibly via the production of a
XX CC vaccine or gene therapy. The current sequence is that of a *Neisseria*
XX CC meningitidis MCS8 outer-membrane vesicle (OMV)-related membrane protein
XX CC of the invention.
XX SQ Sequence 444 AA;

Query Match 52.8%; Score 1300.5; DB 8; Length 444;
Best Local Similarity 57.4%; Pred. No. 5.4e-116;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 35 DVROLLTEIFMKDPEQEFMQAVREAVSLQPVFEKPELLP--PIFKQIVPERVITFRV 92
DB 3 DLNTLFLANKKORNPQEPFHQAVEVPMSLDFFLAKPKYQQSLLEIRVEPVRVFRV 62
QY 93 SWLDAGNLQVNRGFRVQYSSAIGPYKGGIRPHSPVNLSTMKFLAPEQIFKNSLTLLPMG 152
DB 63 TWQDDKGQVQVNRGVRVQVMSAIGPYKGGIRPHFTVDLGVLFKFLAFEQVFKNALTTPLMG 122

QY 153 GKGSSDFDPKGSDAEVMRFQCSFMTLORHISYVQDVPAGDIGVGAREIGYLFQYKR 212
Db 123 GKGSSDFDPKGSDAEVMRFQCSFMTLORHISYVQDVPAGDIGVGAREIGYLFQYKR 182
QY 213 ITKNYTGVLTPKGOEYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 272
Db 183 IRNEFSVLTKGLEWGGSLIRPEATGYGCVYPAQAMLQTRNDSFEGKRVLISGSGNVAQ 242
QY 273 YCAELLEKGAIVLSLSDSQYVYEP-NGFTREQLQAVQDMKKKNNARSISEYKSDTAVY 331
Db 243 YAAEKAIQLCAKVLTVSDSNGFVLPDPSGWTQAALTELKEVRRE-RVATYAKEQGLQ 301
QY 332 VGDRRKPWELDCQVDIAFPCATONEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 391
Db 302 YFEKQKPGV--AAEIALPCATQNELDEAAKTLLANGCYVVAEGANMPSTLGAVEQFIK 359
QY 392 AGIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVDRDKLERIMKDIYDSAMGPSRRY- 450
Db 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEVDRDLFGIMQSIHESCL----KYG 415
QY 451 ----NVDLAAGANIAGFTTKVADAVKAQG 474
Db 416 KVGDTVYVYVNGANIAGFVKVADAMLAQG 443

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Job time : 94.9092 secs

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OM protein - protein search, using sw model

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Title: US-10-627-886-24

Perfect score: 2513

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17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*

18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*

19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*

20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2513	100.0	487	9 US-09-070-844-24	Sequence 24, Appl
2	2513	100.0	487	16 US-10-627-886-24	Sequence 24, Appl
3	2508	99.8	512	9 US-09-070-844-4	Sequence 4, Appl
4	2508	99.8	512	16 US-10-627-886-4	Sequence 4, Appl
5	2508	99.8	526	9 US-09-070-844-2	Sequence 2, Appl
6	2508	99.8	526	16 US-10-627-886-2	Sequence 2, Appl
7	2465	98.1	476	9 US-09-070-844-26	Sequence 26, Appl
8	2465	98.1	476	16 US-10-627-886-26	Sequence 26, Appl
9	1309	52.1	445	15 US-10-282-122A-66687	Sequence 6687, A
10	1300.5	51.8	444	18 US-10-988-943-43	Sequence 43, Appl
11	1297.5	51.6	444	15 US-10-282-122A-65129	Sequence 65129, A

12	1294.5	51.5	444	15	US-10-282-122A-66041	Sequence 66041, A
13	1294.5	51.5	444	15	US-10-275-026A-152	Sequence 152, App
14	1287.5	51.2	449	15	US-10-282-122A-67538	Sequence 67538, A
15	1281	51.0	445	15	US-10-369-493-13947	Sequence 13947, A
16	1259	50.1	454	15	US-10-369-493-9839	Sequence 9839, Ap
17	1257.5	50.0	462	15	US-10-282-122A-45200	Sequence 45200, A
18	1239.5	49.3	448	15	US-10-282-122A-57310	Sequence 57310, A
19	1239.5	49.3	448	18	US-10-953-901-338	Sequence 338, App
20	1238	49.3	449	14	US-10-260-877-90	Sequence 90, Appl
21	1238	49.3	449	15	US-10-282-122A-58096	Sequence 58096, A
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23	1230	48.9	449	15	US-10-282-122A-66870	Sequence 66870, A
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25	1212	48.2	448	17	US-10-472-928-2632	Sequence 2632, Ap
26	1211.5	48.2	448	18	US-10-953-901-340	Sequence 340, App
27	1210.5	48.2	458	15	US-10-369-493-17284	Sequence 17284, A
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32	1201	47.8	447	15	US-10-282-122A-43284	Sequence 43284, A
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36	1194	47.5	438	15	US-10-369-493-10621	Sequence 10621, A
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38	1191	47.4	447	20	US-11-073-550-80	Sequence 80, Appl
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40	1184	47.1	447	20	US-11-073-550-82	Sequence 82, Appl
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42	1181	47.0	447	15	US-10-282-122A-75593	Sequence 75593, A
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44	1180	47.0	447	15	US-10-369-493-295	Sequence 295, App
45	1178	46.9	447	15	US-10-282-122A-72769	Sequence 72769, A

ALIGNMENTS

RESULT 1

US-09-070-844-24

; Sequence 24, Application US/09070844

; Patent No. US20020062495A1

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Robert R.

; APPLICANT: Miller, Philip

; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE

; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/09/070,844

; APPLICATION NUMBER: 08/725,596

; FILING DATE:

; PRIORITY DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Whitlock, Ted W.

; REGISTRATION NUMBER: 36,965

; REFERENCE/DOCKET NUMBER: UF155

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-24

Query Match      100.0%; Score 2513; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.9e-218;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-627-886-24
; Sequence 24, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; APPLICATION NUMBER: 08/725,596
; FILING DATE: 03-OCT-96
; APPLICATION NUMBER: 08/541,033
; FILING DATE: 06-OCT-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: UF-155CD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-627-886-24

Query Match      100.0%; Score 2513; DB 16; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.9e-218;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVSLEEQISAMDATGDTALQKAVQMATKAGTEGLVHGIKNPDVRLQLLTFPMKDPE 60
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QY 481 VKAQGVAV 487
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; Sequence 4, Application US/09070844
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; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-070-844-4

Query Match          99.8%; Score 2508; DB 9; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.2e-217;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      387 CATONEIDEHDAELLIKHGCGYVVEGANMPSNEAIHKYNKAGIYYCPGKAANAGGVAVS 446

; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; APPLICATION NUMBER: 08/725,596
; FILING DATE: 03-OCT-96
; APPLICATION NUMBER: 08/541,033
; FILING DATE: 06-OCT-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: UF-155CD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-10-627-886-4

Query Match          99.8%; Score 2508; DB 16; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.2e-217;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  AVSLEEQISAMDATTTGDFTLQKAVKQMATKAGTEGLVHGINKNPDVRLQLLTFIFMKDPEQ 61
DB      27  AVSLEEQISAMDATTTGDFTLQKAVKQMATKAGTEGLVHGINKNPDVRLQLLTFIFMKDPEQ 86
QY      62  QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVQ 121
DB      87  QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVQ 146
QY      122 YSSAIGPYKGGRLFRHPSVNLIMKFLAFQIIFKNSLTTLPMGGGKGGSDFDPKGSDAEV 181
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QY 302 SOGYVYEPNGFTREOLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAPP 361
Db 327 SOGYVYEPNGFTREOLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAPP 386
QY 362 CATONEIDEHDAELLLKHGCOYVVEGANMPSTNEAIHKYNKAGIITCPGKAANAGGVAVS 421
Db 387 CATONEIDEHDAELLLKHGCOYVVEGANMPSTNEAIHKYNKAGIITCPGKAANAGGVAVS 446
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RESULT 5
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; Sequence 2, Application US/09070844
; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-2

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Query Match 99.8%; Score 2508; DB 9; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.2e-217; Indels 0; Gaps 0;
Matches 486; Conservative 0; Mismatches 0;
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Db 101 QEFMQAVREVAVSLQPVPEKPELLPIPKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQ 160
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Db 341 SOGYVYEPNGFTREOLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAPP 400
QY 362 CATONEIDEHDAELLLKHGCOYVVEGANMPSTNEAIHKYNKAGIITCPGKAANAGGVAVS 421
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RESULT 6
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; Sequence 2, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; APPLICATION NUMBER: 08/725,596
; FILING DATE: 03-OCT-96

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APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-627-886-2

Query Match 99.8%; Score 2508; DB 16; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.2e-217;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVSLEQISAMDATTCGDTALQAVKQMATKAGTEGLVHGINKPDPVRLTTEIFMKDPQ 61
DB 41 AVSLEQISAMDATTCGDTALQAVKQMATKAGTEGLVHGINKPDPVRLTTEIFMKDPQ 100
QY 62 QEFMQAVREAVSLQVPFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQ 121
DB 101 QEFMQAVREAVSLQVPFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQ 160
QY 122 YSAIGPYGGLRPHPSVNLISIMKFLAPQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 181
DB 161 YSAIGPYGGLRPHPSVNLISIMKFLAPQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 220
QY 182 MFCQSFMTLQRLHSYVDVDPAGDIGVAREIGYLFQYKRTKNTYGVLTGPKGOEYGG 241
DB 221 MFCQSFMTLQRLHSYVDVDPAGDIGVAREIGYLFQYKRTKNTYGVLTGPKGOEYGG 280
QY 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLD 301
DB 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLD 340
QY 302 SQGYVPEPFGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPP 361
DB 341 SQGYVPEPFGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPP 400
QY 362 CATONEIDSHDAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVS 421
DB 401 CATONEIDSHDAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVS 460
QY 422 GLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
DB 461 GLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520
QY 482 KAQAV 487
DB 521 KAQAV 526

RESULT 7
US-09-070-844-26
Sequence 26, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
NUMBER OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-070-844-26

Query Match 98.1%; Score 2465; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 8.3e-214;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MDATTGDTALQAVKQMATKAGTEGLVHGINKPDPVRLTTEIFMKDPQBFMQAVREV 71
DB 1 MDATTGDTALQAVKQMATKAGTEGLVHGINKPDPVRLTTEIFMKDPQBFMQAVREV 60
QY 72 AVSLQVPFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVYSSAIGPYKG 131
DB 61 AVSLQVPFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVYSSAIGPYKG 120
QY 132 GLRPHPSVNLISIMKFLAPQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMFQCSFMTTE 191
DB 121 GLRPHPSVNLISIMKFLAPQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMFQCSFMTTE 180
QY 192 LQRHSYVDVDPAGDIGVAREIGYLFQYKRTKNTYGVLTGPKGOEYGGSEIRPEATGY 251
DB 181 LQRHSYVDVDPAGDIGVAREIGYLFQYKRTKNTYGVLTGPKGOEYGGSEIRPEATGY 240
QY 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVPEPNG 311
DB 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVPEPNG 300
QY 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPQATQNEIDSH 371
DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPQATQNEIDSH 360
QY 372 DAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 431
DB 361 DAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
QY 432 LNTWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 487
DB 421 LNTWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 476

RESULT 8
US-10-627-886-26
Sequence 26, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.
 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
 RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE
 DEHYDROGENASES AND METHODS OF USE
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606-6669
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/10/627,886
 APPLICATION NUMBER: US/10/627,886
 FILING DATE: 24-Jul-2003
 CLASSIFICATION DATA: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/070,844
 FILING DATE: 01-MAY-98
 APPLICATION NUMBER: 08/725,596
 FILING DATE: 03-OCT-96
 APPLICATION NUMBER: 08/541,033
 FILING DATE: 06-OCT-95
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: UF-155CD3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 476 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Query Match 98.1%; Score 2465; DB 16; Length 476;
 Best Local Similarity 100.0%; Pred. No. 8.3e-214;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPVRLTLTFMKDPEQBFMQAVREV 71
 DB 1 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPVRLTLTFMKDPEQBFMQAVREV 60
 QY 72 AVSLQPVFKRPPELLIPKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
 DB 61 AVSLQPVFKRPPELLIPKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
 QY 132 GLRFHPSVNLSTLTKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQCSFMT 191
 DB 121 GLRFHPSVNLSTLTKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQCSFMT 180
 QY 192 LQRHSYVQDVDPAGDIGVGAREIGYLFQYKRTKNYTNVGLVFPKQEGYSGSIRPEATGY 251
 DB 181 LQRHSYVQDVDPAGDIGVGAREIGYLFQYKRTKNYTNVGLVFPKQEGYSGSIRPEATGY 240
 QY 252 GAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLLEKCAIVLSLSDSGYVYEPNG 311
 DB 241 GAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLLEKCAIVLSLSDSGYVYEPNG 300
 QY 312 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAPPCCATQNEIDEH 371
 DB 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAPPCCATQNEIDEH 360

QY 372 DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 431
 DB 361 DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420
 QY 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAAGFTTKVADAVKAQGA 487
 DB 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAAGFTTKVADAVKAQGA 476
 RESULT 9
 US-10-282-122A-66687
 ; Sequence 66687, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 66687
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-10-282-122A-66687

Query Match 52.1%; Score 1309; DB 15; Length 445;
 Best Local Similarity 59.2%; Pred. No. 2.8e-109;
 Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;
 QY 47 VRLQLTEIFMKDPEQBFMQAVREVAVSLQPVFKRPPELLP--IPKQIVPEPRVITFRV 104
 DB 5 VDAFLERLKRDDPDQPEPHQAVEEVLRSUMPLEANPHYLEAGIIVERPERALFLRPV 64
 QY 105 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRPHPSVNLSTLTKFLAFQIFKNSLTTLPMGG 164
 DB 65 WYDDQGRVRVNRGFRVQYSSAIGPYKGGLRPHPSVNLSTLTKFLAFQIFKNSLTTLPMGG 124
 QY 165 KGKGSDDPKGKSDAEVMRFQCSFMTLQRHSYVQDVDPAGDIGVGAREIGYLFQYKRI 224

Db 125 GKGSDPDPKGSDAEVRMFCQSPMSLXRVHVGADLDVDPAGDIGVGAREIGYILFGQYKRL 184
QY 225 TKNYTVGLTPKQGEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCVLVSGAGNVAQY 284
Db 185 SNQFTSVLTGKLSYGGSLRPEATGCGVYFAQEMLKDRGRFDGQGVVAISGNNVAQY 244
QY 285 CAELLLKGAIVLSLSDSQGVYVPEPFTREQQAQVDMKKNNARSISEYKSDTAVYVG 344
Db 245 AARKVMEGKGVLSLSDSEGTLYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLQFL 303
QY 345 DRKPWELDCQVDIAFPCATONEIDEHDAELLIKHGQYVVEGANMPSTNEATHKNKAG 404
Db 304 EGRRPWGLAC--DIAUFPATONELDAEDARRLLANGCVCVAEGANMPSTLEAVDLFLEAG 361
QY 405 ILYCPGKAANAGGVAVSGLSMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGPSRRYV 463
Db 362 ILVAPGKASNAGGVAVSGLSEMSQVNRMLRWSGEVDTKLHGIMQSHHACLTYGESQGRV 421
QY 464 DLAAAGNIAGFTKVADAVKAQGV 487
Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

RESULT 10
US-10-988-943-43
; Sequence 43, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; TITLE OF INVENTION: COMPLEX MIXTURES.
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 43
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-43

Query Match 51.8%; Score 1300.5; DB 18; Length 444;
Best Local Similarity 57.4%; Pred. No. 1.6e-108;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;
QY 46 DVRQLLTFIMKDPQEQBFMQAVREAVSLQPVFEKRPPELL--PIFKQIVEPERVITFRV 103
Db 3 DLNTLFANLKKRNPNQEPFHQAVEEVFMSLDPLAKNPKYTOQSLLERIVEPERVVMFRV 62
QY 104 SWLDDAGNLQVNRGVYSSAIGPYKGLRPHSPVNLIMKFLAEPQIFKNSLTPLMG 163
Db 63 TWQDDKGVQVNRGVYVQSSAIGPYKGLRPHSPVNLIMKFLAEPQIFKNSLTPLMG 122
QY 164 GKGSDPDPKGSDAEVRMFCQSPMSLXRVHVGADLDVDPAGDIGVGAREIGYILFGQYK 223
Db 123 GKGSDPDPKGSDAEVRMFCQSPMSLXRVHVGADLDVDPAGDIGVGAREIGYILFGQYK 182
QY 224 ITKNYTVGLTPKQGEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCVLVSGAGNVAQ 283
Db 183 IRNEFSSVLTGKLENGSSLRPEATGCGVYFAQEMLKDRGRFDGQGVVAISGNNVAQ 242
QY 284 YCAELLLKGAIVLSLSDSQGVYVPEPFTREQQAQVDMKKNNARSISEYKSDTAVYVG 344
Db 243 YAAEKAIQLGAKVLTVSDSGFVLPDPSGTEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
QY 343 VGDRRPWLDCQVDIAFPCATONEIDEHDAELLIKHGQYVVEGANMPSTNEATHKNK 402
Db 302 YFEKQKPMGV--AAETALPCATONELDEAAKTLANGCYVVAEGANMPSTLGAVEQFTK 359
QY 403 AGIYCPGKAANAGGVAVSGLSMTQNRMSLNWTRREVRDKLERIMKDIYDSANGPSRRY- 461

Db 360 AGILYAPGKASNAGGVAVSGLSEMSQVNRMLRWSGEVDTKLHGIMQSHHACLTYGESQGRV 421
QY 462 ----NYDLAAGNIAGFTKVADAVKAQGV 485
Db 416 KVGDTVNYVNGANIAGFVKVADAMLAQGV 445

RESULT 11
US-10-282-122A-65129
; Sequence 65129, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 65129
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65129

Query Match 51.6%; Score 1297.5; DB 15; Length 444;
Best Local Similarity 57.4%; Pred. No. 3e-108;
Matches 257; Conservative 70; Mismatches 106; Indels 15; Gaps 6;
QY 46 DVRQLLTFIMKDPQEQBFMQAVREAVSLQPVFEKRPPELL--PIFKQIVEPERVITFRV 103
Db 3 DLNTLFANLKKRNPNQEPFHQAVEEVFMSLDPLAKNPKYTOQSLLERIVEPERVVMFRV 62
QY 104 SWLDDAGNLQVNRGVYSSAIGPYKGLRPHSPVNLIMKFLAEPQIFKNSLTPLMG 163
Db 63 TWQDDKGVQVNRGVYVQSSAIGPYKGLRPHSPVNLIMKFLAEPQIFKNSLTPLMG 122
QY 164 GKGSDPDPKGSDAEVRMFCQSPMSLXRVHVGADLDVDPAGDIGVGAREIGYILFGQYK 223
Db 123 GKGSDPDPKGSDAEVRMFCQSPMSLXRVHVGADLDVDPAGDIGVGAREIGYILFGQYK 182

QY 224 ITKNVTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 283
DB 183 INREFTSVLTGKLEWGGSLIRPEATGYCVYPAQAMLQTRNDSPEGKRVLSGSGNVAQ 242
QY 284 YCAELLLEKGAIVLSLSDSQGYVYBPN-GFTREQLQAVQDMKKKNSARISEYKSDTAVY 342
DB 243 YAAEKAIQIGAKVLTIVSDSDGFVLPDIDGTEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
QY 343 VGDRRKPWELDCQVDIAFFCATQNEIDHDAELLIKHGQYVVEGANMPSTNEATHKYNK 402
DB 302 YFENQKPMGV--AAEIALPCATQNELDEBAKTLTLLANGCYVVAEGANMPSTLGAVEQFIK 359
QY 403 AGIITYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGSPRRY- 461
DB 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVRDQLRFGIMQSHESCL----KYG 415
QY 462 ----NVDLAAGANAGFTTKVADAVKAQ 485
DB 416 KVGDKVNYVNGANIAGFVKVADAMLAQ 443

RESULT 12

US-10-282-122A-66041
; Sequence 66041, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsythe, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
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; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
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; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66041
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria meningitidis

US-10-282-122A-66041

Query Match 51.5%; Score 1294.5; DB 15; Length 444;
Best Local Similarity 57.1%; Pred. No. 5.7e-108;

Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;
QY 46 DVROLLTEIFMKDPEQEFMQAVREVAVSLQPVFEKRPPELL--PIFKOIVPERVITPRV 103
DB 3 DLNTLFAULKORNPQEPFHQAVEVPMSLDPFLAKNPKYQQSLLERIVPERVVMRPRV 62
QY 104 SWLDDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMG 163
DB 63 TWQDDKGGVQVNRGRVQMSAIGPYKGLRPHPTVDLGVLFKFLAFEQVFNKALTTLPMG 122
QY 164 GKGGSDFDPKGSDAEVMRFQSQPMTELRHISYVQVDPAGDIGVGAREIGYLFQGYKR 223
DB 123 GKGGSDFDPKGSDAEVMRFQSQPMTELYRHIGADTDVPAGDIGVGAREIGYLFQGYKK 182
QY 224 ITKNVTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 283
DB 183 IRNEPSSVLTGKLEWGGSLIRPEATGYCVYPAQAMLQTRNDSPEGKRVLSGSGNVAQ 242
QY 284 YCAELLLEKGAIVLSLSDSQGYVYBPN-GFTREQLQAVQDMKKKNSARISEYKSDTAVY 342
DB 243 YAAEKAIQIGAKVLTIVSDSDGFVLPDIDGTEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
QY 343 VGDRRKPWELDCQVDIAFFCATQNEIDHDAELLIKHGQYVVEGANMPSTNEATHKYNK 402
DB 302 YFENQKPMGV--AAEIALPCATQNELDEBAKTLTLLANGCYVVAEGANMPSTLGAVEQFIK 359
QY 403 AGIITYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGSPRRY- 461
DB 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVRDQLRFGIMQSHESCL----KYG 415
QY 462 ----NVDLAAGANAGFTTKVADAVKAQ 485
DB 416 KVGDTVNYVNGANIAGFVKVADAMLAQ 443

RESULT 13

US-10-275-026A-152
; Sequence 152, Application US/10275026A
; Publication No. US2004008770A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Christoph
; TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use
; FILE REFERENCE: GJE-6436
; CURRENT APPLICATION NUMBER: US/10/275,026A
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/GB01/02003
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: GB 0011108.8
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-275-026A-152

Query Match 51.5%; Score 1294.5; DB 15; Length 444;
Best Local Similarity 57.1%; Pred. No. 5.7e-108;

Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;
QY 46 DVROLLTEIFMKDPEQEFMQAVREVAVSLQPVFEKRPPELL--PIFKOIVPERVITPRV 103
DB 3 DLNTLFAULKORNPQEPFHQAVEVPMSLDPFLAKNPKYQQSLLERIVPERVVMRPRV 62
QY 104 SWLDDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMG 163
DB 63 TWQDDKGGVQVNRGRVQMSAIGPYKGLRPHPTVDLGVLFKFLAFEQVFNKALTTLPMG 122
QY 164 GKGGSDFDPKGSDAEVMRFQSQPMTELRHISYVQVDPAGDIGVGAREIGYLFQGYKR 223
DB 123 GKGGSDFDPKGSDAEVMRFQSQPMTELYRHIGADTDVPAGDIGVGAREIGYLFQGYKK 182

QY 224 ITKNYTGVLTPKQOEYGGSEIRPEATGYGAVLFVENVLKDGBSLKKGKCLVSGAGNVAQ 283
Db 183 IRNEFSVLTGKLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSPEGKRVLSGSGNVAQ 242
QY 284 YCAELLEKGAIVLSLSDSGYVYEP-NGFTRELOQAVQDMKKKNSARISEYKSTAY 342
Db 243 YAEKAIQLGAKVLTVSDSNGVLFDPDSGMSAEQLAALIELKEVRRE-RVATYAKEGGJQ 301
QY 343 VGDRRPWELDCQVDIAFPCCATONEIDEHDAELLIKHGCOYVVEGAMFSTNEAIHKYNK 402
Db 302 YPENQKPGV--AAEIALPCATQNELDEEAAKTLANGCVVVAEGANMSTLGAVEQFTK 359
QY 403 AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY- 461
Db 360 AGIIYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVRDQRLFGIMQSIHESCL----KYG 415
QY 462 ---NVDLAAGANIAGFTKVADAVKAQG 485
Db 416 KVGDTVYVNGANIAGFVKVADAMLAQG 443

RESULT 14

US-10-282-122A-67538
; Sequence 67538, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITFA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67538
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-67538

Query Match 51.2%; Score 1287.5; DB 15; Length 449;
Best Local Similarity 58.2%; Pred. No. 2.5e-107;

Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4;
QY 47 VRQLLTELFMKDPEQOEFMQAVREAVSLQPVFEKRPELLP--IPKQIVPERVITFRVS 104
Db 8 VDNFLARLKQDPGPEFHQAVEEVRLTWPLEANPHYLQSGILERRVWEPERAVLFRVS 67
QY 105 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLIMKFLAPEQIFKNSLTTLPMGG 164
Db 68 WYDDQGRVQVNRGFRVQYSSAIGPYKGLRPHPSVNLIMKFLAPEQIFKNSLTSLPMGG 127
QY 165 KGKGSDFDPKGSDAEVMRFQOSFMTLQRHISYVQDYPAGDIGVGAREIGVLFQYKRI 224
Db 128 KGKGSDFDPKGSDAEVMRFQOAFMSELYRHIGADCDVPAGDIGVGAREIGFMFGYKRL 187
QY 225 TKNYTGVLTPKQOEYGGSEIRPEATGYGAVLFVENVLKDGBSLKKGKCLVSGAGNVAQ 284
Db 188 ANQFTSVLTGKMTYGGSLIRPEATGYGCVYFAEMLKXQDKRIDRRVAVSGSGNVAQ 247
QY 285 CAELLEKGAIVLSLSDSGYVYEPNGFTRELOQAVQDMKKKNSARISEYKSDTAVYVG 344
Db 248 AARKVMDLGGKVISLSDSEGLTYAEAGLTDQAWDALMELKNVKR-GRISELAGQFGLEPR 306
QY 345 DRKPEWELDCQVDIAFPCCATONEIDEHDAELLIKHGCOYVVEGAMFSTNEAIHKYNKAG 404
Db 307 KGQTPWSLPC--DIALPCATQNELGAEDARTLLRNGCICVAEGANMPTTLEAVDIFLDAG 364
QY 405 IYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAM--GPSRRYN 462
Db 365 IYIAPGKASNAGGVAVSGLEMSQNAIRLSWTRREVRDQRLFGIMQSIHESCLVHSGEADGR 424
QY 463 VDLAAGANIAGFTKVADAVKAQGAV 487
Db 425 INYKGANIAGFVKVADAMLAQGVV 449

RESULT 15

US-10-369-493-13947
; Sequence 13947, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13947
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13947

Query Match 51.0%; Score 1281; DB 15; Length 445;
Best Local Similarity 58.1%; Pred. No. 9.4e-107;

Matches 258; Conservative 59; Mismatches 121; Indels 6; Gaps 4;
QY 47 VRQLLTELFMKDPEQOEFMQAVREAVSLQPVFEKRPELLP--IPKQIVPERVITFRVS 104
Db 5 VESFLARLKGRDPPDQPEFHQAVEEVRLSWPLEANPHYLTSGILERICEPERAVVFRVS 64
QY 105 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLIMKFLAPEQIFKNSLTTLPMGG 164
Db 65 WYDDQGRVQVNRGFRVQYSSAIGPYKGLRPHPSVNLIMKFLAPEQIFKNSLTSLPMGG 124
QY 165 KGKGSDFDPKGSDAEVMRFQOSFMTLQRHISYVQDYPAGDIGVGAREIGVLFQYKRI 224

Db 125 GKGSDFDPKGSDAEBVMRFCAFMSELYRHIGADVDPAGDIGVGAREIGFLFGQYKEL 184
QY 225 TKNYTCVLTPKQBYGSGSEIRPEATGYGAVLFVENVLKKKGESLKGKRCCLVSGAGNVAQY 284
Db 185 SNQFTSVLTGKMTYGGSLIRPEATGFCGCVYFAEEMLKREQTVEGKRV AISGSGNVAQY 244
QY 285 CAELILLEKGAIVLSLSDSQYVVEPNPGFTREOLQAVQDMKKNNNSARISEYKSDTAVVYG 344
Db 245 AARKVNDLGGKVISLSDSGTLYCERAGLSEEOWLALLELKNVKR-GRISELASAFGLEFR 303
QY 345 DRKPMELDCQVDIAFPPCATONEIDSHDAELLIKHCQYVVEGANNPSTNEAIHKYNKAG 404
Db 304 AGQLPWSLPC--DIALPCATQNELDAESARTLLRNGCVCVAEAGANNPTTLEAVDIFI EAG 361
QY 405 IYCFPKAANAGGVAVSGLEMTONRMSLNWTREEVDRDKLERIMKDIYDSAMG-PSRRYNV 463
Db 362 ILFAPGKASNAGGVAVSGLEMSQNAURLLWTGGEVDSKLHGIMQSIHACVHYGENGRI 421
QY 464 DLAAGANIAGFTKVADAVKAQGAV 487
Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

Search completed: September 8, 2005, 02:38:55
Job time : 92.1268 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2513	100.0	487	2	US-08-541-033A-24	Sequence 24, Appl
2	2513	100.0	487	2	US-08-828-451-24	Sequence 24, Appl
3	2508	99.8	512	2	US-08-541-033A-4	Sequence 4, Appl
4	2508	99.8	512	2	US-08-828-451-4	Sequence 4, Appl
5	2508	99.8	526	2	US-08-541-033A-2	Sequence 2, Appl
6	2508	99.8	526	2	US-08-828-451-2	Sequence 2, Appl
7	2485	98.1	476	2	US-08-541-033A-26	Sequence 26, Appl
8	2485	98.1	476	2	US-08-828-451-26	Sequence 26, Appl
9	1309	52.1	450	4	US-09-252-991A-20646	Sequence 20646, A
10	1257.5	50.0	467	4	US-09-328-352-5725	Sequence 5725, A
11	1234.5	49.1	448	4	US-09-134-000C-3884	Sequence 3884, Ap
12	1221	48.6	448	4	US-09-583-110-4489	Sequence 4489, Ap
13	1201	47.8	447	2	US-08-886-640-3	Sequence 3, Appl
14	1201	47.8	447	3	US-08-884-235-11	Sequence 11, Appl
15	1200	47.8	447	1	US-08-370-193A-11	Sequence 11, Appl
16	1191	47.4	452	4	US-09-489-039A-7937	Sequence 7937, Ap
17	1177.5	46.9	446	4	US-09-543-681A-6657	Sequence 6657, Ap
18	1177	46.8	447	3	US-08-508-761B-6	Sequence 6, Appl
19	1147	45.6	461	3	US-09-171-337A-5	Sequence 5, Appl
20	1147	45.6	461	4	US-09-631-022-5	Sequence 5, Appl
21	1143	45.5	449	1	US-08-831-753-1	Sequence 1, Appl
22	1037.5	41.3	454	4	US-09-538-092-767	Sequence 767, App
23	1012	40.3	368	4	US-09-107-433-4041	Sequence 4041, Ap
24	788.5	31.4	298	4	US-09-248-798A-17483	Sequence 17483, A
25	552.5	22.0	420	3	US-09-134-001C-3103	Sequence 3103, Ap
26	537.5	21.4	374	4	US-09-710-279-2162	Sequence 2162, Ap
27	537	21.4	509	4	US-09-902-540-11352	Sequence 11352, A

QY 61 QQEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRV 120
Db 61 QQEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRV 120
QY 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAE 180
Db 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAE 180
QY 181 VMRFQCSFMTLQRIHSYVQDVDPAGDIGVGAREIGYLFQYKRITKNTYGVLTTPKGQBYG 240
Db 181 VMRFQCSFMTLQRIHSYVQDVDPAGDIGVGAREIGYLFQYKRITKNTYGVLTTPKGQBYG 240
QY 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLS 300
Db 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLS 300
QY 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVVYVDRRKPWELDCQVDIAF 360
Db 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVVYVDRRKPWELDCQVDIAF 360
QY 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCPCGAANAGGVAV 420
Db 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCPCGAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
Db 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
QY 481 VKAQAV 487
Db 481 VKAQAV 487

RESULT 2

US-08-828-451-24
; Sequence 24, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-24
Query Match 100.0%; Score 2513; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.1e-223;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAVSLEEQISAMDATTTGDTALQKAVQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPE 60
Db 1 MAVSLEEQISAMDATTTGDTALQKAVQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPE 60
QY 61 QQEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRV 120
Db 61 QQEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRV 120
QY 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAE 180
Db 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAE 180
QY 181 VMRFQCSFMTLQRIHSYVQDVDPAGDIGVGAREIGYLFQYKRITKNTYGVLTTPKGQBYG 240
Db 181 VMRFQCSFMTLQRIHSYVQDVDPAGDIGVGAREIGYLFQYKRITKNTYGVLTTPKGQBYG 240
QY 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLS 300
Db 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLS 300
QY 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVVYVDRRKPWELDCQVDIAF 360
Db 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVVYVDRRKPWELDCQVDIAF 360
QY 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCPCGAANAGGVAV 420
Db 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCPCGAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
Db 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
QY 481 VKAQAV 487
Db 481 VKAQAV 487
RESULT 3
US-08-541-033A-4
; Sequence 4, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-541-033A-4

Query Match 99.8%; Score 2508; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKPDRVRLQLTEIFMKDPEQ 61
DB 27 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKPDRVRLQLTEIFMKDPEQ 86
QY 62 QEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRVQ 121
DB 87 QEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRVQ 146
QY 122 YSSAIGPYKGLRFPSPVNLISIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 181
DB 147 YSSAIGPYKGLRFPSPVNLISIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 206
QY 182 MRFQCSFMTLORHISYVQDVPAGDIGVGAREIGYLFQGYKRTKNYTGVLTPKGOEYGG 241
DB 207 MRFQCSFMTLORHISYVQDVPAGDIGVGAREIGYLFQGYKRTKNYTGVLTPKGOEYGG 266
QY 242 SEIRPEATGYGAVLFVENLKDGBSLKGRCLVSGAGNVAQYCAELLEKGAIIVLSLD 301
DB 267 SEIRPEATGYGAVLFVENLKDGBSLKGRCLVSGAGNVAQYCAELLEKGAIIVLSLD 326
QY 302 SQGYVPEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFP 361
DB 327 SQGYVPEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFP 386
QY 362 CATQNEIDEHDAELLIKHGQYVVEGANPSTNEAIHKYNKAGIIPCPCANAGGVAVS 421
DB 387 CATQNEIDEHDAELLIKHGQYVVEGANPSTNEAIHKYNKAGIIPCPCANAGGVAVS 446
QY 422 GLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDVAV 481
DB 447 GLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDVAV 506
QY 482 KAQGA 487
DB 507 KAQGA 512

RESULT 4
US-08-828-451-4
Sequence 4, Application US/08828451
Patent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-451-4

Query Match 99.8%; Score 2508; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKPDRVRLQLTEIFMKDPEQ 61
DB 27 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKPDRVRLQLTEIFMKDPEQ 86
QY 62 QEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRVQ 121
DB 87 QEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRVQ 146
QY 122 YSSAIGPYKGLRFPSPVNLISIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 181
DB 147 YSSAIGPYKGLRFPSPVNLISIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 206
QY 182 MRFQCSFMTLORHISYVQDVPAGDIGVGAREIGYLFQGYKRTKNYTGVLTPKGOEYGG 241
DB 207 MRFQCSFMTLORHISYVQDVPAGDIGVGAREIGYLFQGYKRTKNYTGVLTPKGOEYGG 266
QY 242 SEIRPEATGYGAVLFVENLKDGBSLKGRCLVSGAGNVAQYCAELLEKGAIIVLSLD 301
DB 267 SEIRPEATGYGAVLFVENLKDGBSLKGRCLVSGAGNVAQYCAELLEKGAIIVLSLD 326
QY 302 SQGYVPEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFP 361
DB 327 SQGYVPEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFP 386
QY 362 CATQNEIDEHDAELLIKHGQYVVEGANPSTNEAIHKYNKAGIIPCPCANAGGVAVS 421
DB 387 CATQNEIDEHDAELLIKHGQYVVEGANPSTNEAIHKYNKAGIIPCPCANAGGVAVS 446
QY 422 GLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDVAV 481
DB 447 GLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDVAV 506
QY 482 KAQGA 487
DB 507 KAQGA 512

RESULT 5
US-08-541-033A-2
Sequence 2, Application US/08541033A
Patent No. 5879941

```
/ GENERAL INFORMATION:
/ APPLICANT: Schmidt, Robert R.
/ APPLICANT: Miller, Philip
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
/ TITLE OF INVENTION: RELATING TO THE A- AND -SUBUNITS OF GLUTAMATE
/ TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/541,033A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Whitlock, Ted W.
/ REGISTRATION NUMBER: 36,965
/ REFERENCE/DOCKET NUMBER: UF155
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 526 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-541-033A-2
/
/ Query Match          99.8%; Score 2508; DB 2; Length 526;
/ Best Local Similarity 100.0%; Pred. No. 1.3e-222;
/ Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 2 AVSLEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETFMKDPQ 61
/ DB 41 AVSLEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETFMKDPQ 100
/
/ QY 62 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQ 121
/ DB 101 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQ 160
/
/ QY 122 YSSAIGPYKGLRPHSPVNLNLSIMKFLAFAQIKNLSLTTLPMGGGKGSDFDPKGSDAEV 181
/ DB 161 YSSAIGPYKGLRPHSPVNLNLSIMKFLAFAQIKNLSLTTLPMGGGKGSDFDPKGSDAEV 220
/
/ QY 182 MRFCOSFMTLQRHISYQVDPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGOEYGG 241
/ DB 221 MRFCOSFMTLQRHISYQVDPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGOEYGG 280
/
/ QY 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCILVSGAGNVAQYCAELLEKGAIVLSLD 301
/ DB 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCILVSGAGNVAQYCAELLEKGAIVLSLD 340
/
/ QY 302 SQGYVYEPNGFTREQQAQVDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAPP 361
/ DB 341 SQGYVYEPNGFTREQQAQVDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAPP 400
/
/ QY 362 CATQNEIDHDAELLIKHGCQYVVEGANPSTNEAIHKYKAGIICPCKAANAGVAVS 421
/ DB 401 CATQNEIDHDAELLIKHGCQYVVEGANPSTNEAIHKYKAGIICPCKAANAGVAVS 460
/
/ QY 422 GLEMTQNRMSLNTREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
/ DB 461 GLEMTQNRMSLNTREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520
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QY 482 KAQGA 487
DB 521 KAQGA 526

RESULT 6
US-08-828-451-2
/ Sequence 2, Application US/08828451
/ Patent No. 5985634
/ GENERAL INFORMATION:
/ APPLICANT: Schmidt, Robert R.
/ APPLICANT: Miller, Philip
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
/ TITLE OF INVENTION: RELATING TO THE A- AND -SUBUNITS OF GLUTAMATE
/ TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/828,451
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/541,033
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Whitlock, Ted W.
/ REGISTRATION NUMBER: 36,965
/ REFERENCE/DOCKET NUMBER: UF155
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 526 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-828-451-2
```

```
Query Match          99.8%; Score 2508; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 2 AVSLEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETFMKDPQ 61
/ DB 41 AVSLEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETFMKDPQ 100
/
/ QY 62 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQ 121
/ DB 101 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQ 160
/
/ QY 122 YSSAIGPYKGLRPHSPVNLNLSIMKFLAFAQIKNLSLTTLPMGGGKGSDFDPKGSDAEV 181
/ DB 161 YSSAIGPYKGLRPHSPVNLNLSIMKFLAFAQIKNLSLTTLPMGGGKGSDFDPKGSDAEV 220
/
/ QY 182 MRFCOSFMTLQRHISYQVDPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGOEYGG 241
/ DB 221 MRFCOSFMTLQRHISYQVDPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGOEYGG 280
/
/ QY 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCILVSGAGNVAQYCAELLEKGAIVLSLD 301
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Db 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKEGAIIVLSLSD 340
QY 302 SQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAPP 361
Db 341 SQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAPP 400
QY 362 CATONEIDDEDAELLKHGCGQYVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGVAVS 421
Db 401 CATONEIDDEDAELLKHGCGQYVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGVAVS 460
QY 422 GLEMTQNRSLNWTREVRDKLERIMKDIYDSAMGPSRRYVNDVLAAGANIAGFTKVVADAV 481
Db 461 GLEMTQNRSLNWTREVRDKLERIMKDIYDSAMGPSRRYVNDVLAAGANIAGFTKVVADAV 520
QY 482 KAQGA 487
Db 521 KAQGA 526

RESULT 7
US-08-541-033A-26
; Sequence 26, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE A- AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-541-033A-26

Query Match 98.1%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-218;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MDATTGDFALQAVKQMATKAGTEGLVHGKINPDVRLLTETFMKDPQEQFMAQVREV 71
Db 1 MDATTGDFALQAVKQMATKAGTEGLVHGKINPDVRLLTETFMKDPQEQFMAQVREV 60
QY 72 AVSLQVFEKRPPELLPIFQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
Db 61 AVSLQVFEKRPPELLPIFQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120

QY 132 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMCGGKGSGDFDPKGKSDAEVMEFQCSFMTE 191
Db 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMCGGKGSGDFDPKGKSDAEVMEFQCSFMTE 180
QY 192 LORHISYVDVPAGDIGVAREIGYLFQYKEITKNYTGVLTPKQGEYGGSEIRPEATGY 251
Db 181 LORHISYVDVPAGDIGVAREIGYLFQYKEITKNYTGVLTPKQGEYGGSEIRPEATGY 240
QY 252 GAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCAELLEKEGAIIVLSLSDSQGYVYEPNG 311
Db 241 GAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCAELLEKEGAIIVLSLSDSQGYVYEPNG 300
QY 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAPPATQNEIDEH 371
Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAPPATQNEIDEH 360
QY 372 DAELLIKHGCGQYVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGVAVSGLMTQNRMS 431
Db 361 DAELLIKHGCGQYVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGVAVSGLMTQNRMS 420
QY 432 LNWTREVRDKLERIMKDIYDSAMGPSRRYVNDVLAAGANIAGFTKVVADAVKAQGA 487
Db 421 LNWTREVRDKLERIMKDIYDSAMGPSRRYVNDVLAAGANIAGFTKVVADAVKAQGA 476

RESULT 8
US-08-828-451-26
; Sequence 26, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE A- AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-26

Query Match 98.1%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-218;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 12 MDATTGDTALQKAVQMATKAGTEGLVHGIKNPDVROLLTEIFMKDPEQBEFMAQVREV 71
Db 1 MDATTGDTALQKAVQMATKAGTEGLVHGIKNPDVROLLTEIFMKDPEQBEFMAQVREV 60
QY 72 AVSLQPVFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
Db 61 AVSLQPVFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
QY 132 GLRPHSPVNLISIMKFLAFBQIFKNSLTTLPMGGKGGSDPDPKGSDAEFVNRFCQSPMTE 191
Db 121 GLRPHSPVNLISIMKFLAFBQIFKNSLTTLPMGGKGGSDPDPKGSDAEFVNRFCQSPMTE 180
QY 192 LQRHISVQVDPAGDIGVAREIGYLFQGYKRITKNYTVGLTPKQGYGSGSEIRPEATGY 251
Db 181 LQRHISVQVDPAGDIGVAREIGYLFQGYKRITKNYTVGLTPKQGYGSGSEIRPEATGY 240
QY 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 311
Db 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 300
QY 312 FTREQLQAVQDMKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPFCATQNEIDEH 371
Db 301 FTREQLQAVQDMKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPFCATQNEIDEH 360
QY 372 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 431
Db 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420
QY 432 LNWTRREVRDKLRIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 487
Db 421 LNWTRREVRDKLRIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 476

RESULT 9
US-09-252-991A-20646
; Sequence 20646, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20646
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20646

Query Match 52.1%; Score 1309; DB 4; Length 450;
Best Local Similarity 59.2%; Pred. No. 4.4e-112;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 47 VROLLTEIFMKDPEQBEFMAQVREAVSLQPVFEKRPPELLP--IFKQIPEPERVITFRVS 104
Db 10 VDAFLERLKERDDQPEFHQAQVEVLRSLWFFLEAPHYLAEAGIIRIIVEPERAILFRVP 69
QY 105 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLISIMKFLAFBQIFKNSLTTLPMGG 164
Db 70 WVDQGRVVRNRYRVQMSAIGPYKGLRPHSPVNLGLVKLFAEQVFKNLSLTTLPMGG 129
QY 165 GKGSDFDPKGSDAEFVNRFCQSPMTLQRIHISYVQVDPAGDIGVAREIGYLFQGYKRI 224
Db 130 GKGSDFDPKGSDAEFVNRFCQSPMTLQRIHISYVQVDPAGDIGVAREIGYLFQGYKRI 189
QY 225 TKNYTVGLTPKQGYGSGSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 284
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Db 190 SNOQTSVLTGKLSYSGSLIRREATGFCVYFAQEMLKDRGRGFCQORVAISSGQVNAQY 249
QY 285 CAELLLKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKONNSARISEYKSDTAVYVG 344
Db 250 AARKVMEMGGKVISLSDSRGTLTYAEAGLQDEQWEYLMELKNVRR--GRIREMABQFSLQFL 308
QY 345 DRKPKWELDCQVDIAFPFCATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 404
Db 309 EGRRPWGLAC--DIALPFCATQNEIDEHDAEDARRLLANGCVCVAGGANMPSTLEAVDLFEAG 366
QY 405 IICPCPKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLRIMKDIYDSA--WGPSRRYV 463
Db 367 ILYAPKASNAGGVAVSGLEMTQNRMSLNWTRREVRDKLRIMKDIYDSA--WGPSRRYV 426
QY 464 DLAAGANIAGFTKVADAVKAQAV 487
Db 427 NYVKGANIAGFTKVADAVKAQAV 450

RESULT 10
US-09-328-352-5725
; Sequence 5725, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5725
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5725

Query Match 50.0%; Score 1257.5; DB 4; Length 467;
Best Local Similarity 55.9%; Pred. No. 2.6e-107;
Matches 256; Conservative 61; Mismatches 128; Indels 13; Gaps 5;

QY 38 LVH-----GIKNPDVROLLTEIFMKDPEQBEFMAQVREAVSLQPVFEKRPPELLP--IF 89
Db 11 LHYAEDRALKYNLNEFLNYVQARDPHQPEFLQAAVEEVTSLWPFIFSKNPEYAEQGLL 70
QY 90 KOIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLISIMKFLAF 149
Db 71 ERLVEPERVITFRVSWMDQGGQTQVNRAPRVQYNSAIGPFKGMRFPHSPVNLISILKFLGF 130
QY 150 EQIFKNSLTTLPMGGKGGSDPDPKGSDAEFVNRFCQSPMTLQRIHISYVQVDPAGDIGV 209
Db 131 EQTFKNSLTTLPMGGKGGSDPDPKGSDAEFVNRFCQALMIELRYHLRHLGTPNTDIPAGDIGV 190
QY 210 GAREIGYLFQGYKRITKNYTVGLTPKQGYGSGSEIRPEATGYGAVLFVENVLKDGESLK 269
Db 191 GAREVGYMAGMKKLSNDTACVFTGKGISFGSGLMRPEATGYGTVFABEMLKTRGQSPA 250
QY 270 GKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKONNS 329
Db 251 GKTVISISGSGNVAQYAAEKAMFLGAKVVTLSDSNGTVYLKNGFTDBELLAENVLMELKNIKR- 309
QY 330 ARISEYKSDTAVYVGDRRKPWELDCQVDIAFPFCATQNEIDEHDAELLIKHGCOYVVEGAN 389
Db 310 GRISFASKHGFEYEGKTPWHI--PVDIALPCATQNELTGEDAKTLIANGVICVAEGAN 367
QY 390 MPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLRIMK 449
Db 368 MPSTLEAVBHFTEAKTILYAPKASNAGGVAVSGLEMTQNRMSLNWTRREVRDKLRIMK 427
QY 450 IYDSAM--GPSRRYVNDLAAGANIAGFTKVADAVKAQ 485
Db 428 IHANCVRVYTKBEDGTWNYVDGANIAGFTKVADAVKAQ 465
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[illegible]

RESULT 11
 US-09-134-000C-3884
 ; Sequence 3884, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3884
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 US-09-134-000C-3884
 Query Match 49.1%; Score 1234.5; DB 4; Length 448;
 Best Local Similarity 55.9%; Pred. No. 3.2e-105;
 Matches 250; Conservative 63; Mismatches 123; Indels 11; Gaps 6;
 QY 47 VRQLLTFEIMPKDPEQOEFMQAVREVAVSLQPVFEKRPPELLP--IPKQIVPEPVRITFRVS 104
 Db 7 VKNIQEKIHQLDQGTETYLQAVDEFLPTVEGFELEKNPQYIEANVLGLIEFERIFQFRVP 66
 QY 105 WLDDAGNLQVNRGFRVQYSSAIGPYKGLGRFHPHSVNLSSIMKFLAPAEQIFKNSLTTLPMGG 164
 Db 67 WDDQGNMHWNRGFRVQYSSAIGPYKGLGRFHPHSVNLSSIMKFLAPAEQIFKNSLTGLPTGG 126
 QY 165 GKGGSDFDPKGSDAEVMRFQSFMTQLORHISYVQDVPAGDIGVGAREIGYLFQYKRI 224
 Db 127 GKGGSDFDPKGSDAEVMRFQSFMTQLORHISYVQDVPAGDIGVGAREIGYLFQYKRI 186
 QY 225 TKNYTGVLTTPKQOEGYSGSIRPEATGYGAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQY 284
 Db 187 RNYDAGVLTKPLGYGWSQARTATGYGTVYFVKHLLADKNDTFEGKVAVSGSNVAIY 246
 QY 285 CAELLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQDMKKNNNSARISEYKSDT--AVY 342
 Db 247 AMEKATELGATVITSDSGYVYDPEGI---DVALVKELKEKNRE-RISKYVETRKATY 302
 QY 343 VGRDRKPEWLDQVDIAPPCATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNK 402
 Db 303 Y-DKESVMNFETAYDIALPCATQNEINEKQAAIILVKGKVVYVAEGANMPCFLEAVAFK 361
 QY 403 AGIIPCPCGAANAGGAVVAGLEMTQNSLNTWREVRDKLERIMKDIYDSAMGPSRRYN 462
 Db 362 SAVIYCPCGAANAGGAVVAGLEMTQNSLNTWREVRDKLERIMKDIYDSAMGPSRRYN 421
 QY 463 V--DLAAGANIAGFTKVDADVAQAQAV 487
 Db 422 ARDNFVLGANIAGFEKVAAMLSHGLV 448
 RESULT 12
 US-09-583-110-4489
 ; Sequence 4489, Application US/09583110
 ; Patent No. 6695703
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 ; FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
 ; FILE REFERENCE: PATH00-07A
 ; CURRENT APPLICATION NUMBER: US/09/583,110
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/107,433
 ; PRIOR FILING DATE: 1998-06-30

```

; FILING DATE: 01-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,058
; FILING DATE: 02-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul K.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 81163/241766
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-886-640-3

```

```

Query Match          47.8%; Score 1201; DB 2; Length 447;
Best Local Similarity 54.0%; Pred. No. 4e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

```

```

QY 47 VRQLLTETFMKDPQEQBMQAVREAVSLQPVFKRPEL--LPQKQIVPERVITPRVS 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LESFLNHVQKRDPNQTEFAQAQVREVMITLPPLEQNPKYRQMSLLERLVEPERVIQFRV 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 105 WLDAGNLQVNRGFRVQVSSAIGPYKGLRHPSVNLTKFLAPEQIFKNSLTTLPMGG 164
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 WDDRNQIQVNRARVQFSSAIGPYKGMRFPHSVNLSLKPLGPEQTFKNALTTLPWGG 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 KGKGSDFDPKGSDAEVRFCQSPMTELQRIHSYVQDVPAGDIGVGAREIGYLFQYKRI 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 KGKGSDFDPKGSSEGVNRFQALMTLYRLHGLADTDVPAGDIGVGREVGFMAGMMKCL 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 225 TKNTYGVLTTPKQYGGSEIRPEATGYGAVLFVNVLKDKGSLKGRKCLVSGAGNVAQY 284
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 SNTACVFTKGLSFGSLIRPEATGYGLVYFTTEAMLRKHGMFGPMRVSVSGSNVAQY 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 285 CAELLEKGAVLSLSDSGYVVEPNFTREQLQAVQDMKKNSARISEYKSDTAVVVG 344
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 AIEKAMFEGARVITASDSGTVVDSGTFTEKRLARLIEI-KASRDGRVADYAKFGLVYL 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 345 DRKPWELDCQVDIAPPQATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 404
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 EQQPMWSL--PVDIALPCATQNELVDAAHQLIANGVKAEGAANMPTTIEATELFQOAG 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 405 IYCFGKAANAGGAVSGLEMTQNRMSLNTWTRVDRKLERIMKDIYDSAM---GPSRRY 461
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 VLFAPGKAANAGGAVATSGLEMAQNAARLGWKAEKVDARLHLMIDIHACVDHGGEGQT 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 462 NVDLAAGANIAGTQKVAADAKQAGV 487
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 N--YVQGANIAGFVKVADAMLAQGYI 447
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 14
US-08-884-235-11
; Sequence 11, Application US/08884235
; Patent No. 6329573
; GENERAL INFORMATION:
; APPLICANT: Lightfoot, David A.
; APPLICANT: Long, Lynn M.
; APPLICANT: Lightfoot, Maria E. Vidal
; TITLE OF INVENTION: PLANTS CONTAINING THE gdhA GENE AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington

```

```

; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,235
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 residues
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-884-235-11

```

```

Query Match          47.8%; Score 1201; DB 3; Length 447;
Best Local Similarity 54.0%; Pred. No. 4e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

```

```

QY 47 VRQLLTETFMKDPQEQBMQAVREAVSLQPVFKRPEL--LPQKQIVPERVITPRVS 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LESFLNHVQKRDPNQTEFAQAQVREVMITLPPLEQNPKYRQMSLLERLVEPERVIQFRV 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 105 WLDAGNLQVNRGFRVQVSSAIGPYKGLRHPSVNLTKFLAPEQIFKNSLTTLPMGG 164
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 WDDRNQIQVNRARVQFSSAIGPYKGMRFPHSVNLSLKPLGPEQTFKNALTTLPWGG 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 KGKGSDFDPKGSDAEVRFCQSPMTELQRIHSYVQDVPAGDIGVGAREIGYLFQYKRI 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 KGKGSDFDPKGSSEGVNRFQALMTLYRLHGLADTDVPAGDIGVGREVGFMAGMMKCL 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 225 TKNTYGVLTTPKQYGGSEIRPEATGYGAVLFVNVLKDKGSLKGRKCLVSGAGNVAQY 284
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 SNTACVFTKGLSFGSLIRPEATGYGLVYFTTEAMLRKHGMFGPMRVSVSGSNVAQY 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 285 CAELLEKGAVLSLSDSGYVVEPNFTREQLQAVQDMKKNSARISEYKSDTAVVVG 344
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 AIEKAMFEGARVITASDSGTVVDSGTFTEKRLARLIEI-KASRDGRVADYAKFGLVYL 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 345 DRKPWELDCQVDIAPPQATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 404
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 EQQPMWSL--PVDIALPCATQNELVDAAHQLIANGVKAEGAANMPTTIEATELFQOAG 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 405 IYCFGKAANAGGAVSGLEMTQNRMSLNTWTRVDRKLERIMKDIYDSAM---GPSRRY 461
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 VLFAPGKAANAGGAVATSGLEMAQNAARLGWKAEKVDARLHLMIDIHACVDHGGEGQT 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 462 NVDLAAGANIAGTQKVAADAKQAGV 487
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 N--YVQGANIAGFVKVADAMLAQGYI 447
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 15
US-08-370-193A-11
; Sequence 11, Application US/08370193A
; Patent No. 5573945
; GENERAL INFORMATION:
; APPLICANT: ONO, EIJI
; APPLICANT: TSUJIMOTO, NORIHARU
; APPLICANT: MATSUI, KAZUHIKO
; APPLICANT: KURAHASHI, KAZUHIKO
; TITLE OF INVENTION: MUTANT AND METHOD FOR PRODUCING
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.

```


STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,193A
FILING DATE: 09-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-714-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-370-193A-11

Query Match 47.8%; Score 1200; DB 1; Length 447;
Best Local Similarity 54.0%; Pred. No. 4.9e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;
QY 47 VRQLTEIFMKDPEQEEFMQAVREAVSLQPVFEKPEL--LPFKQIVPEPERVITERVS 104
Db 7 LESFLNHVQKDPNQTEFAQAQREVTTLWPLEQNKPYRQMSLLERLVEPERVIOFRVV 66
QY 105 WLDDAGNLQNRGFRVQYSSAIGPYKGLRFPSPVNLISIMKFLAPEQIFKNSLTTLPMGG 164
Db 67 WYDRNQIQVNRARVQFSASIGPYKGNRFHPSVNLISILKFLGFEQTFKNALTLPMGG 126
QY 165 GKGGSDFDPKGSADAFVMPFCQSFMTLQRIHSYVQDVPAGDIGVGAIRIGYLFQYKRI 224
Db 127 GKGGSDFDPKGSSEGEVRFQALMTLYRHLGADTDVPAGDIGVGREVGFMGMMKCL 186
QY 225 TKNYTGVLTTPKGOEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQY 284
Db 187 SNTACVFTGKGLSFGSLIRPEATGYGLVYFTEAMLKKGHGMFGEMRVSVSGSGNVAQY 246
QY 285 CAELLLEKGAIVLSLSDSQGYVVEPNGFTRQLOAQVODMKKNNGARISEYKSDTAVYVG 344
Db 247 ALEKAMEFGARVITASDSSGTVDSESGFTKEKLRLIEI-KASRDGRVADYAKEFGLVYL 305
QY 345 DRKPMELDCQDIAPPQATONEIDHDAELIKHGQCYVVEGANNPSTNEAIHKYNKAG 404
Db 306 EGQQPWLSL--PVDIALPCATQNELDVAHAQLIANGKAVAEAGANNPTTIEATLFFQQAQ 363
QY 405 ILYCPKKAANAGGAVSGLEMTQNRMSLNWTRVEVRDKLERIMKDIYSAM---GPSRRY 461
Db 364 VLFAPKKAANAGGAVTSGLEMPQNAARLGMKAEKVDA RLHHIMLDITHHACVHGGEQQT 423
QY 462 NYDLAAGANIAGFTKVADAVKAQGA 487
Db 424 N--YVQGANIAGFKVADAMLAQGV 447

Search completed: September 8, 2005, 02:12:07
Job time : 27.0834 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 02:12:18 ; Search time 88.1553 Seconds
(without alignments)
2828.902 Million cell updates/sec

Title: US-10-627-886-24

Perfect score: 2513

Sequence: 1 MAVSLEQISAMDAITGDPFT.....GANIAGFTKVDVAKQAGAV 487

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2446	97.3	523	1 DHE4_CHLSO	P28998 chlorella s
2	1375	54.7	510	2 Q81LF7	Q81lf7 plasmodium
3	1361	54.2	1203	2 Q7RQ39	Q7rg39 plasmodium
4	1328	52.8	446	2 Q7VZU9	Q7vzu9 spironucleu
5	1327.5	52.8	449	2 Q7R3N7	Q7r3n7 giardia lam
6	1324.5	52.7	449	1 DHE4_GIALA	P28724 giardia lam
7	1309	52.1	445	2 Q9HVJ7	Q9hvj7 pseudomonas
8	1300.5	51.8	444	2 Q9JY71	Q9jy71 neisseria m
9	1294.5	51.5	444	2 Q9JT56	Q9jt56 neisseria m
10	1287.5	51.2	449	2 Q8RQ23	Q8rq23 pseudomonas
11	1286.5	51.2	470	2 Q9E940	Q9e940 plasmodium
12	1286.5	51.2	470	2 Q81LT0	Q81lt0 plasmodium
13	1285	51.1	445	2 Q9Z3C4	Q9z3c4 pseudomonas
14	1284.5	51.1	437	2 Q7VZU7	Q7vzu7 trichomonas
15	1265	50.3	442	2 Q9TXS8	Q9txs8 plasmodium
16	1264	50.3	442	2 Q9TKS5	Q9tk5 plasmodium
17	1257	50.0	465	2 Q6S143	Q6s143 uncultured
18	1253.5	49.9	536	2 Q7RGT5	Q7rgt5 plasmodium
19	1250.5	49.8	448	2 Q8G6L0	Q8g6l0 bifidobacte
20	1250.5	49.8	455	2 Q8G872	Q8g872 ruminococcu
21	1249.5	49.7	447	2 Q6FD67	Q6fd67 acinetobact
22	1241.5	49.4	448	2 Q8XK85	Q8xk85 clostridium
23	1240.5	49.4	449	2 Q8E4J6	Q8e4j6 streptococc
24	1239.5	49.3	448	2 Q8J5G2	Q8j5g2 enterococcu
25	1238	49.3	449	1 DHE4_HAEIN	P43793 haemophilus
26	1236.5	49.2	449	2 Q8DY77	Q8dy77 streptococ
27	1234	49.1	447	2 Q61083	Q61083 trypanosoma
28	1231.5	49.0	462	2 Q6SWS7	Q6sws7 manheimia
29	1230.5	49.0	449	2 Q8DUL2	Q8dul2 streptococ
30	1230	48.9	449	2 Q9CPJ4	Q9cpj4 pasteurella
31	1225.5	48.8	444	1 DHE3_BACTN	P94598 bacteroides

32	1225	48.7	448	2 Q9AIW1	Q9aiw1 streptococc
33	1214.5	48.3	444	1 DHE4_PRERU	P95544 prevotella
34	1214	48.3	448	2 Q8DPG0	Q8dpg0 streptococ
35	1212	48.2	448	2 Q97QB4	Q97qb4 streptococ
36	1210.5	48.2	458	2 Q9KB34	Q9kb34 bacillus ha
37	1206.5	48.0	447	2 Q7VSN6	Q7vsn6 bordetella
38	1205.5	48.0	424	2 Q9KTN9	Q9ktn9 deinococcus
39	1205.5	48.0	444	2 Q64Q81	Q64q81 bacteroides
40	1205.5	48.0	464	2 Q7WEU7	Q7weu7 bordetella
41	1202	47.8	448	2 Q88XM9	Q88xm9 lactobacill
42	1201	47.8	447	1 DHE4_ECOLI	P00370 escherichia
43	1200.5	47.8	446	2 Q6O9G6	Q6o9g6 trypanosoma
44	1200	47.8	449	2 Q6AJB1	Q6ajb1 desulfotale
45	1199	47.7	443	2 Q97L29	Q97l29 clostridium

ALIGNMENTS

RESULT 1

ID DHE4_CHLSO STANDARD; PRT; 523 AA.

AC P28998;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 29-MAR-2004 (Rel. 43, Last annotation update)

DE NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)

DS (Fragment)

OS Chlorella sorokiniana.

OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;

OX Chlorellaceae; Chlorella.

OC NCBI TaxID=3076;

RP [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92032762; PubMed=1718478;

RA Cock J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;

RT "A nuclear gene with many introns encoding ammonium-inducible

RT chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella

RT sorokiniana.";

RL Plant Mol Biol. 17:1023-1044 (1991).

CC -!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate

CC + NH(3) + NADPH.

CC -!- SUBUNIT: Homo- and heterohexamer of alpha and beta subunits. Both

CC subunits are encoded by the same gene.

CC -!- SUBCELLULAR LOCATION: Chloroplast.

CC -!- INDUCTION: By ammonium

CC -!- PTM: The N-termini of the alpha and the beta chains are blocked.

CC -!- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.

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EMBL; X58832; CAA41636.1; -; ALT_SEQ.

EMBL; X58831; CAA41635.1; -; ALT_SEQ.

PIR; S17949; S17949.

HSP; P24295; LAUP.

InterPro; IPR006095; GLFV dehydrog.

InterPro; IPR006096; GLFV dehydrog_C.

InterPro; IPR006097; GLFV dehydrog_N.

Pfam; PF0208; GLFV dehydrog; 1.

Pfam; PF02812; GLFV dehydrog_N; 1.

PRINTS; PR00082; GLFDHGNASE.

PROSITE; PS00074; GLFV DEHYDROGENASE; 1.

Chloroplast; NADP; Oxidoreductase.

NON_TER 1

ACT_SITE 202 202 By similarity.

SEQUENCE 523 AA; 57529 MW; A35FE730B5FEF974 CRC64;

```
Query Match          97.3%; Score 2446; DB 1; Length 523;
Best Local Similarity 97.5%; Pred. No. 3.9e-161;
Matches 474; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

2 AVSLEQISAMDATGDTALQKAVKQMATKATGTEGLVHGIIKNPDPVRLQLTIFPMKDPBQ 61
38 AKLRSRSPMDATGDTALQKAVKQMATKATGTEGLVHGIIKNPDLRLQLTIFPMKDPBQ 97
DQ
QY 62 QBFMAVRVAVSLQVPFVKRPPELLIPFKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQ 121
DQ 98 QBFMAVRVAVSLQVPFVKRPPELLIPFKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQ 157
DQ
QY 122 YSSALGPYKGLRFPSPVNLSTMKFLAPFQIPKNSITTLPMGGGKGSDFDPKGSDAEV 181
DQ 158 YSSALGPYKGLRFPSPVNLSTMKFLAPFQIPKNSITTLPMGGGKGSDFDPKGSDAEV 217
DQ
QY 182 MFCQSFMTLQHRHSYVQDVDPAGDIGVAREIGVLFQYKRITTKNYTGVLTGKQEGYGG 241
DQ 218 MFCQSFMTLQHRHSYVQDVDPAGDIGVAREIGVLFQYKRITTKNYTGVLTGKQEGYGG 277
DQ
QY 242 SRIPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSLSD 301
DQ 278 SRIPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSLSD 337
DQ
QY 302 SOGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 361
DQ 338 SOGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 397
DQ
QY 362 CATONEIDHDAELAIKHGCOYVVEGANPSTNEAIHKYNKAGIYCPGKAANAGGVAVS 421
DQ 398 CATONEIDHDAELAIKHGCOYVVEGANPSTNEAIHKYNKAGIYCPGKAANAGGVAVS 457
DQ
QY 422 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVVDLAAGANIAGFTKVADAV 481
DQ 458 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVVDLAAGANIAGFTKVADAV 517
DQ
QY 482 KAQAV 487
DQ 518 KAQAV 523

RESULT 2
Q8ILP7 PRELIMINARY; PRT; 510 AA.
AC Q8ILP7;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase, putative.
GN ORFNames=PF14_0286;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Augioli S.,
RA Perteaux M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrall B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum";
RL Nature 419:498-511(2002).
DR EMBL; AB014820; AAN36899.1; -.
DR HSSP; P24295; IAU.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.

DR InterPro; IPR006096; GLFV dehydrog C.
DR InterPro; IPR006097; GLFV dehydrog N.
DR Pfam; PF02082; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog N; 1.
DR PRINTS; PR00082; GLFV dehydrog.
DR PROSITE; PS00074; GLFV dehydrog.
SQ SEQUENCE 510 AA; 57343 MW; AC400045297AC64F CRC64;

Query Match          54.7%; Score 1375; DB 2; Length 510;
Best Local Similarity 60.0%; Pred. No. 6.7e-87;
Matches 267; Conservative 66; Mismatches 104; Indels 8; Gaps 5;

QY 47 VRQLLTETFMKDPQOEPMQAVRVAVSLQVPFVKRPPELLIPFKQIVPEPRVITFRVSWL 106
DQ 70 IEELREKVVSKNKNPEFLQAFEEVLSCLKPVFKKONVYIGVLENIAPERVIQPRVPMI 129
DQ
QY 107 DDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAPFQIPKNSITTLPMGGGK 166
DQ 130 NDKGEHKNRGRFRVQYNSVLPFYKGLRFPSPVNLSTMKFLAPFQIPKNSITTLPMGGGK 189
DQ
QY 167 GGSDFDPKGSDAEVNMFQSFMTLQHRHSYVQDVDPAGDIGVAREIGVLFQYKRITK 226
DQ 190 GGSDFDPKGSDAEVNMFQSFMTLQHRHSYVQDVDPAGDIGVAREIGVLFQYKRITK 249
DQ
QY 227 NYTGVLTGKQEGYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCA 286
DQ 250 SPFGVLTGKNTKMGGSNIRAEATGYGVVYFAENVLKDNDLENKCKLVSGSGNVAQYLV 309
DQ
QY 287 ELLEKGAIVLSLSDSGYVVEGANPSTNEAIHKYNKAGIYCPGKAANAGGVAVS 344
DQ 310 EKLKGAIVLTGSDSGYVVEGANPSTNEAIHKYNKAGIYCPGKAANAGGVAVS 367
DQ
QY 345 DRRKPWELDCQVDIAPPQATQNEIDHDAELAIKHGCOYVVEGANPSTNEAIHKYNKAG 404
DQ 368 ENQKPMNIP--DIAFPQATQNEIDHDAELAIKHGCOYVVEGANPSTNEAIHKYNKAG 425
DQ
QY 405 ILYCPGKAANAGGVAVSGLNTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRY--N 462
DQ 426 ILYCPGKAANAGGVAVSGLNTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRY--N 485
DQ
QY 463 VDLAAGANIAGFTKVADAVKAQAV 487
DQ 486 SDLVAGANIAGFTKVADAVSFLQGG 510

RESULT 3
Q7RQ39 PRELIMINARY; PRT; 1203 AA.
AC Q7RQ39;
DT 01-MAR-2004 (TremBLrel. 26, Created)
DT 01-MAR-2004 (TremBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=PY01264;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RA PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Augioli S.V., Suh B.B., Kooij T.W., Perteaux M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kozack D.S., Shumway M.P., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii";
```

RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABL01000331; EAA20557.1; -.
DR HSSP: P24295; 1AUP.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR InterPro: IPR005135; Exo endo phos.
DR InterPro: IPR006095; GLFV dehydrog.
DR InterPro: IPR006096; GLFV dehydrog C.
DR InterPro: IPR006097; GLFV dehydrog_N.
DR Pfam: PF03372; Exo endo phos; 1.
DR Pfam: PF02812; GLFV dehydrog; 1.
DR PRINTS: PR00082; GLFV dehydrog N; 1.
DR PROSITE: PS00074; GLFV dehydrogenase; 1.
SQ SEQUENCE 1203 AA; 13909 MW; DBE1988BD4C21715 CRC64;

Query Match 54.2%; Score 1361; DB 2; Length 1203;
Best Local Similarity 59.3%; Pred. No. 1.9e-85;
Matches 264; Conservative 65; Mismatches 108; Indels 8; Gaps 5;

QY 47 VRQLLTETFWKDEQEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVRVITFRVSWL 106
Db 763 IEMKENVISKNDQHEFLQAFEEVLTSLKPVFKNIYYLGVLENISEPVRVQPRVPMI 822

QY 107 DDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGK 166
Db 823 NDNGEHKINRGFRVQYSSVILGPKYKGLRPHPTVNLISVIRKPLFQEFKNSLTTLPMGGGK 882

QY 167 GGSDFDPKGSDAEVMRFQCSFMTELQRIHSYVDVPAGDIGVAREIGYLFQGYKRIITK 226
Db 883 GGSDFDPKGSNEILLRFQCSFMDELFRYIGPNTDIPAGDIGVAREIGYLFQGYKRIITK 942

QY 227 NTGVLTPKQGVGSEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQYCA 286
Db 943 KFEGLVTGKNIKGGSGNIRSEATGYGAVFAENALSDMNEKNTKCVSGSGNVAQYLV 1002

QY 287 ELLLEKGAIVLSLSDSQYVYVPEPNGFTREQLQAVQDMKKNSARISEY--KSDTAVYV 344
Db 1003 ELLLEKGAIVLSLSDSQYVYVPEPNGFTREQLQAVQDMKKNSARISEY--KSDTAVYV 344

QY 345 DRKRPWELDQVDIAFPFCATQNEIDHDAELIKHGCGQYVVEGANMPSNEAIHKYKAG 404
Db 1061 ENKEPNVFC--DIVFPFCATQNEITENDADLLIKNCKLLVSGANMPTIKAWHKLKENK 1118

QY 405 ILYCPGKAANAGGAVSGLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGFSRRY--N 462
Db 1119 ILICPSKAANAGGAVSGLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGFSRRY--N 462

QY 463 VDLAAGANTAGFTKQADAVKAQAV 487
Db 1179 TDLVAGANTAGFLKQADSFIEQGG 1203

RESULT 4
QY7ZU9 ID Q7Y7ZU9 PRELIMINARY; PRT; 446 AA.
AC Q7Y7ZU9
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
DE Glutamate dehydrogenase (Fragment).
GN Name=gdh;
OS Spiroplasma barchanensis.
OC Eukaryota; Diplomonadida; Hexamitidae; Hexamitinae; Spiroplasma.
OX NCBI_TaxID=103874;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 50380;
RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;
RA Andersson J.O., Roger A.J.;

RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene
RT transfer within and between prokaryotes and eukaryotes.";
RL BMC Evol. Biol. 3:14-14 (2003).
DR EMBL: AF533884; AAP83851.1; -.
DR HSSP: P24295; 1AUP.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR InterPro: IPR006095; GLFV dehydrog.
DR InterPro: IPR006096; GLFV dehydrog C.
DR InterPro: IPR006097; GLFV dehydrog_N.
DR Pfam: PF02812; GLFV dehydrog; 1.
DR Pfam: PF02812; GLFV dehydrog N; 1.
DR PROSITE: PS00074; GLFV dehydrogenase; 1.
SQ SEQUENCE 446 AA; 49309 MW; AEB43D2A1762DB80 CRC64;

Query Match 52.8%; Score 1328; DB 2; Length 446;
Best Local Similarity 58.6%; Pred. No. 1e-83;
Matches 262; Conservative 65; Mismatches 110; Indels 10; Gaps 6;

QY 46 DVROLLETFWMDPEQEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVRVITFRVSW 105
Db 5 DKNVLLQ---RDANIEFCQAVNEIDSLTVFEENPKYISVFQELLEPERVIMFRVPM 61

QY 106 LDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGG 165
Db 62 TDDKGEVINRGYRQYNSALGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGG 121

QY 166 KGSDFDPKGSDAEVMRFQCSFMTELQRIHSYVDVPAGDIGVAREIGYLFQGYKRIIT 225
Db 122 KGSDFDPKGSNGEVMRFQCSFMTELQRIHSYVDVPAGDIGVAREIGYLFQGYKRIIT 181

QY 226 KNYTGLTPKQGVGSEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQYCA 285
Db 182 NOFTGILTKGAYSWGSGSLRPEATGYGAVLYNEMWLDNGDDIKGRVLLSGAGNVAQYCA 241

QY 286 AELLLEKGAIVLSLSDSQYVYVPEPNGFTREQLQAVQDMKKNSARISEY--KSDTAVYV 343
Db 242 TEKLLHYGAIPLSLSDSNGTIIENPGFTAEQLKQVMDLKNIKR-CRLSEYTSMSSTAKY 300

QY 344 GDRKRPWELDQVDIAFPFCATQNEIDHDAELIKHGCGQYVVEGANMPSNEAIHKYK 402
Db 301 -EGQRPWAVYEGVDVIMPCATQNEVNGTEAEVIRKGLRYVSEGANMPSNDDAIHAYHS 359

QY 403 AGIYCPGKAANAGGAVSGLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGFSRRY 462
Db 360 SKVYFGPAKAGGAVSGLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGFSRRY 419

QY 463 VDLAAGANTAGFTKQADAVKAQAV 487
Db 420 KKNYQFGANAGFLKQADSMIDQCCV 446

RESULT 5
QY7R3N7 ID Q7R3N7 PRELIMINARY; PRT; 449 AA.
AC Q7R3N7
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 39 39379 38030.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

422 NYVKGANIAGFVKVADAMLAQGVV 445

RESULT 8

Q9JY71 PRELIMINARY; PRT; 444 AA.

ID Q9JY71

AC Q9JY71

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Glutamate dehydrogenase, NADP-specific.

GN OrderedLocusNames=NMB1710.

OS Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

NCBI_TaxID=491;

FN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MC58 / Serogroup B;

RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;

RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,

RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,

RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,

RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,

RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,

RA Cifton H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,

RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,

RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,

RA Venter J.C.;

RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain

RT MC58.";

RL Science 287:1809-1815(2000).

DR EMBL; AE002521; AAF42057.1; .

DR PTR: H81050; H81050.

DR HSP; P24295; IAU.

DR TIGR; NMB1710; .

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006520; P:amino acid metabolism; IEA.

DR InterPro; IPR006095; GLFV_dehydrog.

DR InterPro; IPR006096; GLFV_dehydrog C.

DR InterPro; IPR006097; GLFV_dehydrog N.

DR Pfam; PF00208; GLFV_dehydrog; 1.

DR Pfam; PF02812; GLFV_dehydrog N; 1.

DR PRINTS; PR00082; GLFV_DEHYDROGNASE.

DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.

KW Complete proteome.

SQ SEQUENCE .444 AA; 48490 MW; 8B2FCCA89EF7DAF CRC64;

Query Match 51.8%; Score 1300.5; DB 2; Length 444;

Best Local Similarity 57.4%; Pred. No. 8.2e-82;

Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

Qy 46 DVHQQLLTEIPMKDPDEQEFMQAVREAVSLQPFVKEPELL--PIFQIIVEPERVIIFRV 103

Db 3 DLNTLFLANLKQRPNQSPFPQAEVEEVPMSLDPLAKNPKYTQOSLLERIVEPERVVMFRV 62

Qy 104 SWLDDAGNLQVNGFRVQYSSAIGPYKGLRHPSVNLSTMKTLAFQIIFKNSLTLLPMG 163

Db 63 TWQDDKQGVQVNGIRVQMSAIGPYKGGURFHTVDLGLKFLAFQVQFNALTLLPMG 122

Qy 164 GKGGSDFDPKGSDAEWMRFCSQFMTELQRHISYYVDVPAGDITGVGAREIGYLFQYKR 223

Db 123 GKGGSDFDPKGSDAEWMRFQAFMTELYRHIGADTDVPAGDITGVGAREIGYLFQYKK 182

Qy 224 ITKNYGVLTTPKQOYGGSIIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 283

Db 183 IRNEFSSVLTKGLEWGGSLIRPEATGYGCVFAQAMLQTRNDSFEGRVLLISGSGNVAQ 242

Qy 284 YCAELLLEKCAIVLSLSDSGGYVEP--NGFTRELQAVQDMKKKNSARISEYKSDTAVY 342

Db 243 YAAEKAIQLGAKVLTVSDSNGVFLFPPSGMTEAQLAALIIEKVRRE-RVATYAKEQGLQ 301

Qy 343 VGRRRKPEWLDQVDIAFPACATQNEIDEHDAEALLIKHGCOYVVEGANPSPNEAIHKYNK 402

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Db 302 YFEKQKPGV--AAEIALPCATQNELDEBAKTLANGCYVVAEGANPSTLIGAVEQPIK 359
QY 403 AGIICYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAMGPSRRY- 461
Db 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVDQRLFGIMQSHESCL-----KYG 415
QY 462 ----NVDLAAGANIAGFTKVADAVKAQG 485
Db 416 KVGDTVNVYNGANIAGFVKVADAMLAQG 443

RESULT 9
Q9JUT56 PRELIMINARY; PRT; 444 AA.
AC Q9JUT56;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase (EC 1.4.1.4).
GN Name=gdhA; OrderedLocuNames=NM11964;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies K.M., Davis P., Devlin K., Feltwell T., Hamlin K.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491."
RC Nature 404:502-506 (2000).
DR EMBL; AL162757; CAB85184.1; -.
DR F1R; B81825; B81825.
DR HSSP; P24295; 1AUP.
DR GO; GO:0004354; P:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF0208; GLFV_dehydrog_N.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 444 AA; 48462 MW; DE7F1A7B8DD6F424 CRC64;

Query Match 51.5%; Score 1294.5; DB 2; Length 444;
Best Local Similarity 57.1%; Pred. No. 2.1e-81;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 46 DVRQLLTETFMKDPQOEPMQAVRVAVSLQVFEKRPPELL--PIFKQIVPERVITPRV 103
Db 3 DLNLTLPANLKQNPQEPHQAVEEVPMSLDPFLAKNPKYTOQSLLERIVEPERVVMFRV 62
QY 104 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAPFQIFKNSLTPLMG 163
Db 63 TWQDDKGQVQNRGRVQYSSAIGPYKGLRPHPSVNLISIMKFLAPFQIFKNSLTPLMG 122
QY 164 GSKGSDPDPKGSDAEVMRFQCSFWTELQHSYVQVDPAGDIGVAREITGLFGQYKR 223
Db 123 GSKGSDPDPKGSDAEVMRFQCSFWTELQHSYVQVDPAGDIGVAREITGLFGQYKR 182
QY 224 ITKNTGVLTTPKQBYGSGSEIRPEATGVAVLFEVNLKDKGSLKGRCLVSGAGNVAQ 283
Db 183 IRNEFFSSVLTGKLEWGGSLIRPEATGVAVLFEVNLKDKGSLKGRCLVSGAGNVAQ 242

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QY 284 YCAELLEKGAIIVLSLDSQGYVYEP-NGFTREQLQAVQDMKKNNNSARISEYKSDTAVY 342
Db 243 YAAEKATQLGAKVLTVSDSNGFVLPDPSGMSAQALALIELKVRRE-RVATYAKEQGLQ 301
QY 343 VGDRRKQWELDCQVDIAPPCCATONEIDEHDAELLIKHCQVYVVEGANNPSTNEAIHKYNK 402
Db 302 YFENQKPGV--AAEIALPCATQNELDEBAKTLANGCYVVAEGANPSTLIGAVEQPIK 359
QY 403 AGIICYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAMGPSRRY- 461
Db 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVDQRLFGIMQSHESCL-----KYG 415
QY 462 ----NVDLAAGANIAGFTKVADAVKAQG 485
Db 416 KVGDTVNVYNGANIAGFVKVADAMLAQG 443

RESULT 10
Q88Q23 PRELIMINARY; PRT; 449 AA.
AC Q88Q23;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=gdhA; OrderedLocuNames=PP0675;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfle E.K., Scanlan D., Tran K.,
RA Moazzes A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eissen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AE016776; AAN66300.1; -.
DR HSSP; P24295; 1AUP.
DR TIGR; PP0675; -.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF0208; GLFV_dehydrog_N; 1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 48871 MW; EF1733B6ABC89627 CRC64;

Query Match 51.2%; Score 1287.5; DB 2; Length 449;
Best Local Similarity 58.2%; Pred. No. 6.7e-81;
Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4;

QY 47 VRQLLTETFMKDPQOEPMQAVRVAVSLQVFEKRPPELL--PIFKQIVPERVITPRV 104
Db 8 VDNFLARLKQRPDQPEPHQAVEEVLTPFLANPHYLOSGLERAVEPERAVLFRVS 67
QY 105 WLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAPFQIFKNSLTPLMG 164
Db 68 WVDQDGQVQNRGRVQYSSAIGPYKGLRPHPSVNLISIMKFLAPFQIFKNSLTPLMG 127

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QY 165 GKGSDPDKGSDAEVMPFCQSFMTTELQRHISYYVDVPAGDIGVGAREIGYLFQGYKRI 224
Db 128 GKGSDPDKGSDAEVMPFCQAFMSLYRRHIGADCDVPAGDIGVGAREIGFMFGQYKRL 187
QY 225 TKNYTGVLTPKGOEYCGSIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQY 284
Db 188 ANOFTSVLTGKMTYGGSLRPEATGYGCVYFAEMLKFKQDKRIDRRVAVSGSGNVAQY 247
QY 285 CAELLEKEGAIVLSLSDSQYVYPNGFTREQLQAVQDMKKNNKSARISEYKSDTAVYVG 344
Db 248 AARKVMDLGGKVISLSDSEGLTYAEAGLTDQWDLALMELKNYKR-GRISELAQGCLFPR 306
QY 345 DRKPWELDCQVDIAPPQATONEIDHDAELLKHGCGYVVEGANMPSNEAIIHKYNKAG 404
Db 307 KGOTWPSLPC--DIALPCATQNELGAEDARTLLRNGCICVAEGANMPTTLEAVDIFLDAG 364
QY 405 ILYCPKKAANAGVAVSGLEMTQNRMSLANWTREYVDKLERIMKDIYDSAM--GPSRRYN 462
Db 365 ILYAPKASNAGVAVSGLEMSQNAWRLLTWGTAGEVDSKLHINMQSIHHACVHYGEADGR 424
QY 463 VDLAAGANIAGFTKVADAVKAQAV 487
Db 425 INVKGANIAGFTKVADAMLAQGVV 449

RESULT 11
O96940 PRELIMINARY; PRT; 470 AA.
AC O96940;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
GN Name=GludH; Synonym=GDH;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99089647; PubMed=9874251;
RA Wagner J.T., Iuedemann H., Faerber P.M., Lottspeich F.,
RA Krauth-Siegel R.L.;
RT "Glutamate dehydrogenase, the marker protein of Plasmodium falciparum.
RT Cloning, expression and characterization of the malarial enzyme.";
RL Eur. J. Biochem. 258:813-819(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Li L.H., Li M., Wu Y.S., Wang P.;
RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; Y12927; CAA73390.1; -.
DR EMBL; AY040586; AAK77969.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF00208; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog; 1.
DR PRINTS; PR00082; GLFDHNRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

Query Match 51.2%; Score 1286.5; DB 2; Length 470;
Best Local Similarity 55.2%; Pred. NO. 8.3e-81;
Matches 266; Conservative 64; Mismatches 133; Indels 19; Gaps 7;

QY 9 ISAMDATGDTALQAKVQMATKAGTEGLVHGINKPVDVRLQLTEIFMKDPEQQEFMQAV 68
Db 1 NSGALKDKTRGFVLDK-----NASNYESLV-----DQEMNNVYERVMKLDPNQVBFLOAF 50
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QY 69 REVAVSLQVFEKRPPELLPIPKQIYVEPERVITFRVSWLDDAGNLQVNRGFRVQYSAIGP 128
Db 51 HEILYSLKPLFMEEBPKYLPITETLSEPERAIQFRVCLDDNGVQRKNCRFRVQYNSALGP 110
QY 129 YKGLRFPSPVNLSTMKFLAPBQIFKNSITLTPMGCGGKGGSDFPDKGSDAEVMPFCQSF 188
Db 111 YKGLRFPSPVNLSTVKFLGPEQIFKNSLTGLSMGGGKGGSDFPDKGSDNEILKPCQAF 170
QY 189 MTELQRHISYYVDVPAGDIGVGAREIGYLFQGYKRIITKNYTGVLTPKGOEYCGSIRPEA 248
Db 171 MNELYRHIGPCPTDVPAGDIGVGAREIGYLYGYKKIIVNSFNGTLTGKVNKWSNLVPEA 230
QY 249 TGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKEGAIVLSLSDSQYVYE 308
Db 231 TGYGLVYFVLEVLKSLNIPVEKQTAVVSGSGNVALYCVQKLLHLNVKVLTLSDSNGYVYE 290
QY 309 PNGFTREQLQAVQDMKKNNKSARISEY--KSDTAVYVGDVRRKRWELDCQVDIAFCATON 366
Db 291 PNGFTHEMLEFLIDLKEE-KKGRIKEYLNMHSSTAKYF-PNEKPMGVPC--TLAAPPATON 346
QY 367 EIDEHDAELLKHGCGYVVEGANMPSNEAIIHKYNKAGIYCPKKAANAGVAVSGLEMT 426
Db 347 EINLEDAKLLQKNGCILVEGANMPSVTDAINLFKSNIIYCPKKAANAGVAVSGLEMS 406
QY 427 QNRMSLANWTREYVDKLERIMKDIYDSAMGPSRRY---NVDLAAGANIAGFTKVADAVKA 483
Db 407 QNFQPSHWTRVDEKLEIMRNIFACSENALKYTKNKYDLQAGANIAGFLKVAESYE 466
QY 484 QG 485
Db 467 QG 468

RESULT 12
Q8ILTO PRELIMINARY; PRT; 470 AA.
AC Q8ILTO;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NADP-specific glutamate dehydrogenase.
GN ORFNames=PF14_0164;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Frazer C.M., Barrell B.
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014818; AAN36776.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog C.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF00208; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog_N; 1.
DR PRINTS; PR00082; GLFDHNRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
DR SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;
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[illegible]

Search completed: September 8, 2005, 02:43:30
Job time : 90.1553 secs

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RESULT 15
Q9TXS8
ID Q9TXS8 PRELIMINARY; PRT; 442 AA.
AC Q9TXS8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=GDH;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=FCQ 27;
RC
RA Yuan P., Stewart T.S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098675; AAD11789.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPRO06095; GLFV dehydrog.
DR InterPro; IPRO06096; GLFV dehydrog. C.
DR InterPro; IPRO06097; GLFV dehydrog_N.
DR Pfam; PF02028; GLFV dehydrog; 1.
DR Pfam; PF02813; GLFV dehydrog; 1.
DR PRINTS; PR00082; GLFDHGRNAS.
DR

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:27:13 ; Search time 21.1308 Seconds
(without alignments)
2217.496 Million cell updates/sec

Title: US-10-627-886-24
Perfect score: 2513
Sequence: 1 MAVSLEEQISAMDATTGDTFT.....GANTIAGTKVADAKAQAQAV 487

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2446	97.3	523	1 S17949	glutamate dehydrog
2	1324.5	52.7	449	1 A2489	glutamate dehydrog
3	1309	52.1	445	2 H83072	glutamate dehydrog
4	1300.5	51.8	444	2 H81050	glutamate dehydrog
5	1294.5	51.5	444	2 B81825	glutamate dehydrog
6	1238	49.3	449	2 A64053	glutamate dehydrog
7	1214.5	48.3	444	2 T10487	glutamate dehydrog
8	1214	48.3	448	2 D98019	glutamate dehydrog
9	1212	48.2	448	2 H95151	glutamate dehydrog
10	1210.5	48.2	458	2 E83912	NADP-specific glut
11	1205.5	48.0	424	2 E75362	glutamate dehydrog
12	1201	47.8	447	1 DEBCE	glutamate dehydrog
13	1199	47.7	443	2 F96990	NADP-specific glut
14	1198	47.7	447	2 C90937	NADP-specific glut
15	1198	47.7	447	2 G85785	NADP-specific glut
16	1189.5	47.3	458	2 A11503	NADP-specific glut
17	1185	47.2	447	2 S32227	glutamate dehydrog
18	1182	47.0	447	1 A33504	glutamate dehydrog
19	1181	47.0	447	1 AF0710	NADP-specific glut
20	1180.5	47.0	458	2 A11144	NADP-specific glut
21	1153	45.9	447	2 AE0483	glutamate dehydrog
22	1150	45.8	448	2 D64567	glutamate dehydrog
23	1143	45.5	450	2 S22403	glutamate dehydrog
24	1142.5	45.5	448	2 B95277	probable glutamate
25	1139	45.3	448	2 F71862	glutamate dehydrog
26	1133.5	45.1	446	2 S06938	glutamate dehydrog
27	1121.5	44.6	454	1 DENCEN	glutamate dehydrog
28	1115.5	44.4	459	1 S04904	glutamate dehydrog
29	1109	44.1	457	2 S63608	glutamate dehydrog

30	1092	43.5	451	2 T41492	probable glutamate
31	1067.5	42.5	459	2 S17907	glutamate dehydrog
32	1037.5	41.3	454	1 A25275	glutamate dehydrog
33	1022	40.7	457	2 S51960	glutamate dehydrog
34	997.5	39.7	624	2 B96556	hypothetical prote
35	579.5	23.1	416	2 T45284	glutamate dehydrog
36	576.5	22.9	416	2 G72305	glutamate dehydrog
37	552.5	22.0	421	2 F83852	glutamate dehydrog
38	551	21.9	424	2 A70055	glutamate dehydrog
39	545.5	21.7	426	2 G89933	glutamate dehydrog
40	544.5	21.7	414	2 G89862	NAD-specific gluta
41	536	21.3	372	2 G84220	glutamate dehydrog
42	530	21.1	420	2 D75176	glutamate dehydrog
43	529.5	21.1	430	2 F83989	glutamate dehydrog
44	527.5	21.0	420	2 F84142	glutamate dehydrog
45	527.5	21.0	421	2 B81079	glutamate dehydrog

ALIGNMENTS

RESULT 1

S17949
glutamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fragment)
N/Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C/Species: Chlorella sorokiniana
C/Date: 30-Jun-1992 #sequence revision 23-Mar-1995 #text_change 09-Jul-2004
C/Accession: S17949; S17950; S19030
R/Cock, J.M.; Kim, K.D.; Miller, P.W.; Hutson, R.G.; Schmidt, R.R.
Plant Mol. Biol. 17, 1023-1044, 1991
A/Title: A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP
A/Reference number: S17949; MUID:92032762; PMID:1718478
A/Accession: S17949
A/Molecule type: DNA
A/Residues: 1-523 <COC>
A/Cross-references: UNIPROT:P28998; EMBL:X58831
A/Accession: S17950
A/Molecule type: mRNA
A/Residues: 1-523 <COC>
A/Cross-references: EMBL:X58832; NID:gl8272; PIDN:CAA41636.1; PID:gl8273
R/Schmidt, R.R.
submitted to the EMBL Data Library, April 1991
A/Reference number: S19030
A/Accession: S19030
A/Molecule type: DNA
A/Residues: 1-219, 'LW', 222-523 <SCH>
A/Cross-references: EMBL:X58831
C/Genetics:
A/Genome: nuclear
A/Introns: 6/2; 29/1; 40/3; 56/3; 85/3; 127/3; 149/3; 175/1; 183/3; 211/1; 246/1; 272/2;
C/Superfamily: glutamate dehydrogenase (NAD(P+))
C/Keywords: chloroplast; hexamer; NADP; oxidoreductase
F/202/Binding site: substrate (lys) #status predicted

Query Match		97.3%	Score 2446;	DB 1;	Length 523;
Best Local Similarity		97.5%	Pred. No. 1.5e-173;		
Matches 474;		Conservative 3;	Mismatches 9;	Indels 0;	Gaps 0;
QY	2	AVSLEEQISAMDATTGDTFTALQKAVQMATKAGTEGLVHGINKPNDVRLQLTEIFMKDPEQ	61		
Db	38	AKRLRSRPRMDATTGDTFTALQKAVQMATKAGTEGLVHGINKPNDVRLQLTEIFMKDPEQ	97		
QY	62	QEFQAVREAVSLQPVFEKRPPELLLPFKQIVPEPVRTTFVSWLDDAGNLQVNRGFRVQ	121		
Db	98	QEFQAVREAVSLQPVFEKRPPELLLPFKQIVPEPVRTTFVSWLDDAGNLQVNRGFRVQ	157		
QY	122	YSSAIGPVKGLRPHPSVNLIMKFLAPEQIFKNSLTTLPMGGGKGGSDFPKGSDAEV	181		
Db	158	YSSAIGPVKGLRPHPSVNLIMKFLAPEQIFKNSLTTLPMGGGKGGSDFPKGSDAEV	217		
QY	182	MRFCQSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRIITKNYTGVLTPKQGEYGG	241		
Db	218	MRFCQSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRIITKNYTGVLTPKQGEYGG	277		

QY 242 SEIRPEATGYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCAELLLEKGAIVLSLD 301
DB 278 SEIRPEATGYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCAELLLEKGAIVLSLD 337
QY 302 SQGYVEPNFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 361
DB 338 SQGYVEPNFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 397
QY 362 CATONEIDEHDAELLIKHGCGVYVEGANMPSTNEAIHKYNKAGIIYCPKAAAGGVAVS 421
DB 398 CATONEIDEHDAELLIKHGCGVYVEGANMPSTNEAIHKYNKAGIIYCPKAAAGGVAVS 457
QY 422 GLEMTQNRMSLNMTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
DB 458 GLEMTQNRMSLNMTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 517
QY 482 KAQGAV 487
DB 518 KAQGAV 523
RESULT 2
A:Accession: A42489
N:Alternate names: glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Giardia lamblia
C:Species: Giardia lamblia
C:Date: 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
A:Accession: A42489
R:Yee, J.; Dennis, P.P.
J. Biol. Chem. 267, 7539-7544, 1992
A:Title: Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene
A:Reference number: A42489; MUID:92218410; PMID:1559991
A:Accession: A42489
A:Molecule type: DNA
A:Residues: 1-449 <YEE>
A:Cross-references: UNIPROT:P28724; GB:M84604; NID:g159108; PID:AAA29155.1; PID:g159109
A:Note: sequence extracted from NCBI backbone (NCBI:94071, NCBI:P94074)
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
C:Keywords: NADP; oxidoreductase
F:125/Binding site: substrate (Lys) #status predicted
Query Match 52.7%; Score 1324.5; DB 1; Length 449;
Best Local Similarity 58.2%; Pred. No. 1.9e-90;
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5;
QY 47 VRQLLETFMKDPEQQEFMQAVREAVASLQPVFEKRPPELLPTFKQIVPERVITFRVSWL 106
DB 6 IEELAVIKQRDGHMTEFRQAVEEVVDSLVKVFEREKYPYIPFERMLPERVITFRVPM 65
QY 107 DDAGNLQVNRPRVQYSSAIGPYKGLRPHSPVNSIMKFLAFEQIFKNSLTTLPMGGGK 166
DB 66 DDAGRNVRPRVQYNSALGPYKGLRPHSPVNSILKFLGFEQILKNSLTTLPMGGGK 125
QY 167 GGSDFDPKGSDAEVMRCQSPMTLQRIHSVQDVPAGDITGVGAREIGYLFQYKRI 226
DB 126 GGSDFDPKGSNEVMRCQSPMTLQRIHVADTDVPAGDITGVGAREIGYLFQYKRLN 185
QY 227 NYTGVLTTPKGQBYGSGEIRPEATYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCA 286
DB 186 EFTGVLTGKVKWGGSFIRPEATYGAVYFLBEMCKDNTVIRGNVLLSGSNVAQFAC 245
QY 287 ELLLEKGAIVLSLDSQGYVEPNFTREQLQAVQDMKKKNSARISEYKS---DTAVYV 343
DB 246 EKLIQLGAKVLTFSDSNGTIVDKDGFNEBKLAHMLYLNKGR-GRVSFVKDYPSPVAYE 304
QY 344 GDRRPWE-LDCQVDIAFPCCATONEIDEHDAELLIKHGCGVYVEGANMPSTNEAIHKYNK 402
DB 305 G--KKPWEFCFEGQMCIMPCATQNSVSGDDATRLVGLGLKFVAEGANMPSTAEAVHVYHA 362
QY 403 AGIICYCPKAAAGGVAVSGLGEMTQNRMSLNMTREVRDKLERIMKDIYDSAMGPSRRYN 462
DB 363 KGVMTGPAKASNAGGVAVSGLGEMSQNSVRLQWTAEEVDQKLRGINRGIFVACRDTAKYVG 422

QY 463 --VDLAAGANTAGFTKVADAVKAQAV 487
DB 423 HPKNYQMGANTAGFLKVADSMIEQGV 449
RESULT 3
HB3072
glutamate dehydrogenase PA4588 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
A:Accession: H83072
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <STO>
A:Cross-references: UNIPROT:Q9HVJ7; GB:AE004872; GB:AE004091; NID:g9950829; PIDM:AAG0797
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: gdhA; PA4588
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
Query Match 52.1%; Score 1309; DB 2; Length 445;
Best Local Similarity 59.2%; Pred. No. 2.6e-89;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;
QY 47 VRQLLETFMKDPEQQEFMQAVREAVASLQPVFEKRPPELLP--IFKQIVPERVITFRVS 104
DB 5 VDAFLERKRDRDPQEPHFQAVEVLRSLWPFLEANPHYLEAGIIRIVEPERAILFRVP 64
QY 105 WLDDAGNLQVNRPRVQYSSAIGPYKGLRPHSPVNSIMKFLAFEQIFKNSLTTLPMGG 164
DB 65 WDDQGRVRVNRGVRVQMSAIGPYKGLRPHSPVNSLGLVLFKFLAFEQYFKNSLTTLPMGG 124
QY 165 KGGSDPDPKGSDAEVMRCQSPMTLQRIHSVQDVPAGDITGVGAREIGYLFQYKRI 224
DB 125 KGGSDPDPKGSDAEVMRCQSPMSELYRHVGADLDVPAGDITGVGAREIGYLFQYKRL 184
QY 225 TKNYTVLTTPKGQBYGSGEIRPEATYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQY 284
DB 185 SNQFTSVLTGKLSYGGSLIRPEATGFCGYFAQEBMLKDRGDFGQGVATSGSGNVAQY 244
QY 285 CAELLLEKGAIVLSLDSQGYVEPNFTREQLQAVQDMKKKNSARISEYKSDTAVYV 344
DB 245 AARKVMEGKGKVISLSDSSEGLTYAEAGLSDBQWELMELKNVRR-GRIREMAEQFSLOFL 303
QY 345 DRRKPWELDCQVDIAFPCCATONEIDEHDAELLIKHGCGVYVEGANMPSTNEAIHKYNKAG 404
DB 304 EGRAPWGLAC--DIALPCATQNEIDAEARLLANGCVCVAEGANMPSTLEAVDLFLEAG 361
QY 405 IICYCPKAAAGGVAVSGLGEMTQNRMSLNMTREVRDKLERIMKDIYDSA-MGPSRRYV 463
DB 362 ILVAPGRASNAGGVAVSGLGEMSQNAMRLRWSEGEVDTKLHGIMQSIHHACLLYGEQGRV 421
QY 464 DLAAGANTAGFTKVADAVKAQAV 487
DB 422 NYVKGANTAGPVKVADAMLAQGV 445
RESULT 4
HB1050
glutamate dehydrogenase, NADP-specific NMB1710 [imported] - Neisseria meningitidis (stra
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
A:Accession: H81050
R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81050
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-444 <TET>
A;Cross-references: UNIPROT:Q9JY71; GB:AE002521; GB:AE002098; NID:g7226962; PIDN:AAF4205
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1710
C;Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 51.8%; Score 1300.5; DB 2; Length 444;
Best Local Similarity 57.4%; Pred. No. 1.1e-88;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 46 DVRLQLTEIFMKDPEQEFMQAVREAVASLQPVFEKRPPELL--PIFKQIYVEPERVITFRV 103
DB 3 DLNLTFAANLKQRPNQEPFHQAEEVFMSLDPLAKNPKYTOQSLLERIVEPERVVMFRV 62

QY 104 SWLDDAGNLQVNRGRFVQYSSAIGPYKGGRLRPHPSVNLIMKFLAEPQIFKNSLTTLPMG 163

DB 63 TWQDDRGQVQVNRGRVQVMSAIGPYKGGRLRPHPTVDLGLVLAPEQVFKNALTTLPWG 122

QY 164 GKGGSDFDPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGVLFQYK 223

DB 123 GKGGSDFDPKGSDAEVMRFQCAFMTLYRHRIGADTVDPAGDIGVGREIGVLFQYK 182

QY 224 ITKNYTVGLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 283

DB 183 IRNEPSSVLTKGLEWGGSLIRPEATGYCVVFAQAMLQTRNDSPEGKVLISGSGNVAQ 242

QY 284 YCAELLLKGAIVLSLSDSQYVYEP-NGFTREQLQAVQDMKKNSARISEYKSDTAVY 342

DB 243 YAAEKAIQLGAKVLTVDSDNGFVLPDPSGWTQAALAEITELKEVRR-RVATYAKEQGLQ 301

QY 343 VGDRRKPWELDCQVDIAPCATQNEIDHDAELLIKHGCOYVVEGANMPSTNEAIHKYNK 402

DB 302 YFEKQKPGV--AAEIALPCATQNELDEAAKTLTANGCVVVAEGANMPSTLGAVEQFIK 359

QY 403 AGIYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVDKRLERIMKDIYDSAMGPSRRY- 461

DB 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVDQRLFGIMQSIHESCL----KYG 415

QY 462 ----NVDLAAGANIAGFTTKVADAVKAQ 485

DB 416 KVGDTVNVYNGANIAGFVKVADAMLAQ 443

RESULT 5

B81825
Glutamate dehydrogenase (NADP) (EC 1.4.1.4) NMA1964 [imported] - *Neisseria meningitidis*
C;Species: *Neisseria meningitidis*
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81825
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-444 <PAR>
A;Cross-references: UNIPROT:Q9J7T56; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CB8518
A;Experimental source: serogroup A, strain Z2491

C;Genetics:
A;Gene: gdhA; NMA1964
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: oxidoreductase

Query Match 51.5%; Score 1294.5; DB 2; Length 444;
Best Local Similarity 57.1%; Pred. No. 3.1e-88;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 46 DVRLQLTEIFMKDPEQEFMQAVREAVASLQPVFEKRPPELL--PIFKQIYVEPERVITFRV 103
DB 3 DLNLTFAANLKQRPNQEPFHQAEEVFMSLDPLAKNPKYTOQSLLERIVEPERVVMFRV 62

QY 104 SWLDDAGNLQVNRGRFVQYSSAIGPYKGGRLRPHPSVNLIMKFLAEPQIFKNSLTTLPMG 163

DB 63 TWQDDRGQVQVNRGRVQVMSAIGPYKGGRLRPHPTVDLGLVLAPEQVFKNALTTLPWG 122

QY 164 GKGGSDFDPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGVLFQYK 223

DB 123 GKGGSDFDPKGSDAEVMRFQCAFMTLYRHRIGADTVDPAGDIGVGREIGVLFQYK 182

QY 224 ITKNYTVGLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 283

DB 183 IRNEPSSVLTKGLEWGGSLIRPEATGYCVVFAQAMLQTRNDSPEGKVLISGSGNVAQ 242

QY 284 YCAELLLKGAIVLSLSDSQYVYEP-NGFTREQLQAVQDMKKNSARISEYKSDTAVY 342

DB 243 YAAEKAIQLGAKVLTVDSDNGFVLPDPSGWTQAALAEITELKEVRR-RVATYAKEQGLQ 301

QY 343 VGDRRKPWELDCQVDIAPCATQNEIDHDAELLIKHGCOYVVEGANMPSTNEAIHKYNK 402

DB 302 YFEKQKPGV--AAEIALPCATQNELDEAAKTLTANGCVVVAEGANMPSTLGAVEQFIK 359

QY 403 AGIYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVDKRLERIMKDIYDSAMGPSRRY- 461

DB 360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVDQRLFGIMQSIHESCL----KYG 415

QY 462 ----NVDLAAGANIAGFTTKVADAVKAQ 485

DB 416 KVGDTVNVYNGANIAGFVKVADAMLAQ 443

RESULT 6

A64053
Glutamate dehydrogenase (NADP) (EC 1.4.1.4) - *Haemophilus influenzae* (strain Rd KW20)
C;Species: *Haemophilus influenzae*
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A64053
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman,
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64053
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-449 <TIGR>
A;Cross-references: UNIPROT:P43793; GB:U32704; GB:L42023; NID:gl573143; PIDN:AAC21858.1;
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: NADP; oxidoreductase

Query Match 49.3%; Score 1238; DB 2; Length 449;
Best Local Similarity 55.6%; Pred. No. 5e-84;
Matches 247; Conservative 64; Mismatches 117; Indels 16; Gaps 5;

QY 51 LTFEPMKDPQEQEFMQAVREAVASLQPVFEKRPPELL--PIFKQIYVEPERVITFRVSWLDD 108

DB 11 LTKVAQRDGYQPEFIQAVREVFTSIWPLEANPKYRSEALLERLVEPERAFQFVATWDD 70

QY 109 AGNLQVNRGRFVQYSSAIGPYKGGRLRPHPSVNLIMKFLAEPQIFKNSLTTLPMGGGKG 168

DB 71 KGQVQVNRFAFRVQFNSAIGPFKGGMRPHPSVNLISLKFELGFEQIFKNALTTLPMGAKGG 130

QY 169 SDFDPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGVLFQYKRTKNY 228

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
son, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506. 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95151
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <KUR>
A;Cross-references: UNIPROT:Q97QB4; GB:AE005672; PIDN:AAK75409.1; PID:g14972791; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SPI306
C;Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 48.2%; Score 1212; DB 2; Length 448;
Best Local Similarity 55.5%; Pred. No. 4.2e-82;
Matches 247; Conservative 63; Mismatches 127; Indels 8; Gaps 4

Qy	47 VRQLLTFIMKDPQQEFMQAVREVAVSLQPVFKEKPELLP--IFKVIVPEPVITFRVS 104
Db	8 IQSVFTVKARNGHEAEFLQAVESEFNTLEFPVEFKHPYEENILARTIPERVVSRVP 67

Qy 105 WLDDAGNLQVNRGRFRVQSSAIGPYKGGGLRHFHPSVNLSIMKFLEAQIFKNSLTTLPMGG 164
 | : - : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Dd 68 WVDGDKLVNRRGYRVQFNSAVGPYKGGGLRFHPFTVQGILKFLGEQIFKNVLGTLP IGG 127

Qy	165 GKGSDFDPKGGDAEVMRFCSFMTLQRHISVVDVPAGDIGVGAREGYLFQYKRI 224
Db	128 GKGSDFDPKGGTDAEVMRFCSFMTLQKHIGPSLDVPAGDIGVGGREGYLYGQYKRL 187

Qy	225	TKNYTGVLT	PKGBYGG	SIRPEAT	GYGAVL	FVENVL	KDKGSL	KRCLV	SGAGN	VAQ	284
		:		:		:		:		:	
Db	188	NQFDAGVLT	GKPLFGG	SLIRPEAT	GYGLVY	THEML	KANGNS	PAGK	VWISG	SGN	247
		:		:		:		:		:	

Qy 285 CAELLLLEKGAIVLSLSDSGQVYVPNGFTREQLQAVQDMKKNNNSARISFYKSDTAVVVG 344

Db 248 ALQKATELGATVTSVSDSGYVIDENGI--DFDLLVDVYKEKRR--ARLTGVAAEKATATY 303

Qy 345 DRKPWELDCQVDIAFPQATQNEIDHDAELLIKHGCVYVEGANMPSTNEAIHKYNKAG 404

D_b 304 HECTVTWYAGNYDIALPCATQNEINGEAAKRLVAGVICVSEGANMPSDLDIAIKYKENG 363

Qy 405 IYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVDRKLERIMKDIDYSANGPSPRYNV - 463
| | | | | | | | | | : | : | | | | | : | : | : | : | : | : | :
Db 364 IFYGPAKANAGGVAVSALEMSONSLRLSWTREEVDGRUKDITNIINFNTAKTTSETYGLD 423

Qy

464 -DLAAGANIAGFTKVADAVKAQGAV 487
| | | | | : | |
Dd

424 KDYLAGANIAAFENVVANAMIAQGIV 448

RESULT 10
E83912
NAP-specific glutamate dehydrogenase gdhA [imported] - Bacillus halodurans (strain C-12)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: E83912

Kusakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hara, N. *Nucleic Acids Res.* 28, 4317-4331, 2000

A;Accession: E83512
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <STO>
A;Cross-references: UNIPROT:Q9KB34; GB:BA001514; GB:BA000004; NID:G10174613; PIDN:BA05058
A;Experimental source: strain C-125

C;Genetics: A;Gene: *gdhA*
C;Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match	48.2%;	Score 1210.5;	DB 2;	Length 458;
Best Local Similarity	54.7%;	Pred. No. 5.6e-82;		
Matches 252;	Conservative 71;	Mismatches 121;	Indels 17;	Gaps 7

[illegible]

Qy	92	I V E P E R V I T F R Y S W L D D A G N L Q V N R G F R V Q Y S S A I G P Y K G G L R H P S V N L S I M K L A F E Q	151
		: : : :	
Db	64	I V E P E R V I S F R Y P V W D D Q G V Q V N R G F R V Q F N S A L G P Y K G G L R H P S V N A S I I K E L G F E Q	123

[illegible]

QY
212 REIGVLPFGQYKRITKNY-TGVLTPKQGQYGGSEIRPEATGYGAVLFVENVLKKGESLKG 270
:
Db
184 KEIYMFGQYKKORGGFPEAGVLTCKGTGCGGSLARKEATGYGTVTYFVEENIKDHGFSPAG 243

QY 271 KRCLVSGAGNVAQYCAELLEKGAVLSLSDSGSYVYPNGFTREQQAQVDMKKNSA 330
244 STVWSSGNSIYAMEKAMQLGAKVACSDSGSYVDKNGIDLQTVKRLKEVERK--- 299
Db

331 RISEYNEHFAHYVQCGSIWSVPC--DIALPCATQNELDEAAATMLANGVRAVGEGA 357

QY ||||| : :: | : ||||| : ||||| : |||||
389 NMFSTNEALHKRYNKAGILYCYPGKAANAGGVASGLEMTQNRMSLNWTREVRDKLERIMK 440

Db 358 NMPSTLQAVHFPQEHEGVLFAPAKAANAGGVSALEMAQNSTRLAWTFPEEVDAKIYEIMK 417

QY	449	DIYDSAMGFSKRRINVV--DLAAGANIAGFTKVADAVRAQGAV	487
		: :: :	
Dd	418	NIYRESIKAAELVEASGNLVVGANIAGFVKVADAMISHGVV	458

RESULT 11
F75362

glutamate dehydrogenase - *Deinococcus radiodurans* (strain R1)

C;Species: *Deinococcus radiodurans*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: E/5362
R/White, O.; Eisen, J.A.; Heidelber, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Accession: E75362
A;Reference number: A75230; MOLD:20030896; FMID:1036726
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-424 <WHI>

A;Cross-references: UNIPROT:Q9RTH1

A;Experimental source: strain RI
C:Genetics.

A;Gene: DRI

A;Map position: 1

C;Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 48.0%: Score 1205.5: DB 2: Length 424:

Best Local Similarity	56.2%;	Pred. No. 1.2e-81;	
Matches	240;	Conservative	61; Mismatches 119; Indels 7; Gaps 4

[illegible]

Qy 123 SSAIGPYKGLRPHPSVNLSIMKFLAEQIFKNLSLTILPMGGKGGSDDPKGKSDAEVM 182
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
c1 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

DB 61 SSSIGPYKGGMRFFHPSVNLSILKFLAFEQITFKNALITLPLGGKGGSDFDPRGKSDGEVM 120

Db 244 ANQKATQLGAKVAVMSDSNGYIYDANGINLNTIRKIKVERK-----RIHEYTKYHPNASY 299

Qy 343 VGDRRKPWELDCOVDTIAPPCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNK 402

Db 300 TEGCDGIMWKLK--DIALPCATONEIDENSAKTLIANGCYAVCEGANMESTIEAVDLFTK 357

Qy 403 AGIIYCPGKAANAGGVAVSGLEWMTQNRMSLNWTRREVRDKLERIMKDIYDSANGPSRRYN 462

Db 358 NKVIFGPKAANAGGVATSALEMSQNSMRYSTFEEDVKLQINIMKNIYIKCSNAANEYG 417

Qy 463 VD--LAAGANIAGFTKVADAVKAQG 485

Db 418 FEDNLVAGANIAGFTKVACAMYSLG 442

RESULT 14

C90937

NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub C90937

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: C90937

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference sequence A95629; PMID:11258796

A:Accession: C90937

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-447 <HAY>

A:Cross-references: UNIPROT:Q8XDW9; GB:BA000007; PIDN:BA835890.1; PID:gi3361934; GSPDB:G

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs2467

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 47.7%; Score 1198; DB 2; Length 447;

Best Local Similarity 53.8%; Pred. No. 4.6e-81;

Matches 240; Conservative 68; Mismatches 128; Indels 10; Gaps 5;

Qy 47 VRQLLTFIMKDPQEQEFMQAVREAVLSQPVFEKRPDL--LPFQKQIVEPERVITFRVS 104

Db 7 LESFLNHVQKRDPNQTEFAQAVREVMVTLWPFLEQNPKYRQMSLLERLVEPERVIOFRV 66

Qy 105 WLDAGNLQVNRGFRVQVSSAIGPYKGLRPHSPVNSIMKFLAPEQIFKNSLTTLPMGG 164

Db 67 WDDRNQVQVNRVQVSSAIGPYKGMRFHPSVNLKPLGFLGPEQTFKNAITLPMGG 126

Qy 165 KGKGSDFDPKGSDAEVMRFQCSFMTELQRIHSYVQDVPAGDIGVGAREIGVLFQYKRI 224

Db 127 KGKGSDFDPKGSSEGEVNRFCQALMTELYRHLGADTVDPAGDIGVGGREVGFMAGMMKKL 186

Qy 225 TKNYTGVLTTPKQEGYSGSIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 284

Db 187 SNNTACVFTGKLSFGGSLIRPEATGYGLVYFTTEAMLKRHGMFGFEGMRVSVSGSGNVAQY 246

Qy 285 CAELLEKGAIVLSLSDSGYVYVPPNGFTREOLQAVQDMKKNSARISEYKSDTAVVYG 344

Db 127 KGKGSDFDPKGSSEGEVNRFCQALMTELYRHLGADTVDPAGDIGVGGREVGFMAGMMKKL 186

Qy 225 TKNYTGVLTTPKQEGYSGSIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 284

Db 187 SNNTACVFTGKLSFGGSLIRPEATGYGLVYFTTEAMLKRHGMFGFEGMRVSVSGSGNVAQY 246

Qy 285 CAELLEKGAIVLSLSDSGYVYVPPNGFTREOLQAVQDMKKNSARISEYKSDTAVVYG 344

Db 247 ALEKAMEFGARVITASDSSGTVDSESGTKEKRLARLIEI-KSSRDGRVADYAKERGLVYL 305

Qy 345 DRKPWELDCOVDTIAPPCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 404

Db 306 EGQOPMSV--PVDIALPCATQNELDVDAHQIANGVKAEGANMPTTIEATELFFQOAG 363

Qy 405 IYCPGKAANAGGVAVSGLEWMTQNRMSLNWTRREVRDKLERIMKDIYDSAM---GPSRRY 461

Db 364 VLPFAPGKAANAGGVATSGLEMAQNAARLGWKAERKVDARLHMLDIHHACVHGEGEQT 423

Qy 462 NVDLAAGANIAGFTKVADAVKAQGAV 487

Db 424 N--YVQGANIAGFVKVADAMLAQGV 447

RESULT 15

G85785

NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: G85785

R:Perina, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; PMID:21074935; PMID:11206551

A:Accession: G85785

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-447 <STO>

A:Cross-references: UNIPROT:Q8XDW9; GB:AE005174; NID:gi2515786; PIDN:AA056747.1; GSPDB:G

A:Experimental source: strain O157:H7, substrain EDJ933

C:Genetics:

A:Gene: gdhA

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 47.7%; Score 1198; DB 2; Length 447;

Best Local Similarity 53.8%; Pred. No. 4.6e-81;

Matches 240; Conservative 68; Mismatches 128; Indels 10; Gaps 5;

Qy 47 VRQLLTFIMKDPQEQEFMQAVREAVLSQPVFEKRPDL--LPFQKQIVEPERVITFRVS 104

Db 7 LESFLNHVQKRDPNQTEFAQAVREVMVTLWPFLEQNPKYRQMSLLERLVEPERVIOFRV 66

Qy 105 WLDAGNLQVNRGFRVQVSSAIGPYKGLRPHSPVNSIMKFLAPEQIFKNSLTTLPMGG 164

Db 67 WDDRNQVQVNRVQVSSAIGPYKGMRFHPSVNLKPLGFLGPEQTFKNAITLPMGG 126

Qy 165 KGKGSDFDPKGSDAEVMRFQCSFMTELQRIHSYVQDVPAGDIGVGAREIGVLFQYKRI 224

Db 127 KGKGSDFDPKGSSEGEVNRFCQALMTELYRHLGADTVDPAGDIGVGGREVGFMAGMMKKL 186

Qy 225 TKNYTGVLTTPKQEGYSGSIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 284

Db 187 SNNTACVFTGKLSFGGSLIRPEATGYGLVYFTTEAMLKRHGMFGFEGMRVSVSGSGNVAQY 246

Qy 285 CAELLEKGAIVLSLSDSGYVYVPPNGFTREOLQAVQDMKKNSARISEYKSDTAVVYG 344

Db 247 ALEKAMEFGARVITASDSSGTVDSESGTKEKRLARLIEI-KSSRDGRVADYAKERGLVYL 305

Qy 345 DRKPWELDCOVDTIAPPCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 404

Db 306 EGQOPMSV--PVDIALPCATQNELDVDAHQIANGVKAEGANMPTTIEATELFFQOAG 363

Qy 405 IYCPGKAANAGGVAVSGLEWMTQNRMSLNWTRREVRDKLERIMKDIYDSAM---GPSRRY 461

Db 364 VLPFAPGKAANAGGVATSGLEMAQNAARLGWKAERKVDARLHMLDIHHACVHGEGEQT 423

Qy 462 NVDLAAGANIAGFTKVADAVKAQGAV 487

Db 424 N--YVQGANIAGFVKVADAMLAQGV 447

Search completed: September 8, 2005, 02:44:38

Job time : 23.1308 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:10:02 ; Search time 96.0793 Seconds
(without alignments)
1960.383 Million cell updates/sec

Title: US-10-627-886-24

Perfect score: 2513

Sequence: 1 MAVSLREQISAWDATGDTFT.....GANTIAGFTKVADAVKQAQAV 487

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 38760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2513	100.0	487	5	Aau98954 Mature NA
2	2513	100.0	487	8	Adq36729 Mature NA
3	2508	99.8	512	2	Aaw15408 NADP-spec
4	2508	99.8	512	5	Aau98951 NADP-glut
5	2508	99.8	512	8	Adq36709 NADP-spec
6	2508	99.8	526	2	Aaw15407 NADP-spec
7	2508	99.8	526	5	Aau98950 NADP-glut
8	2508	99.8	526	8	Adq36707 NADP-spec
9	2505	99.7	487	2	Aaw15411 NADP-spec
10	2465	98.1	476	2	Aaw15412 NADP-spec
11	2465	98.1	476	5	Aau98955 Mature NA
12	2465	98.1	476	8	Adq36731 Mature NA
13	1309	52.1	445	6	Abu38763 Protein e
14	1309	52.1	450	7	Abu71900 Pseudomon
15	1300.5	51.8	444	8	Adp08330 Neisseria
16	1297.5	51.6	444	6	Abp77942 N. gonorr
17	1297.5	51.6	444	6	Abu37205 Protein e
18	1294.5	51.5	444	5	Aau72986 Neisseria
19	1294.5	51.5	444	6	Abu38117 Protein e
20	1287.5	51.2	449	6	Abu39614 Protein e
21	1281	51.0	445	8	Adq24914 Bacterial
22	1259	50.1	454	8	Adm27186 Bacterial
23	1257.5	50.0	462	6	Abu17276 Protein e
24	1257.5	50.0	467	6	Ada34438 Acinetoba
25	1250.5	49.8	448	5	Abp65630 Bifidobac

ALIGNMENTS

RESULT 1

AAU98954

ID AAU98954 standard; protein; 487 AA.

AC AAU98954;

DT 24-SEP-2002 (first entry)

DE Mature NADP-glutamate dehydrogenase alpha subunit.

XX NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.

OS Chlorella sorokiniana.

PN US2002062495-A1.

PD 23-MAY-2002.

PF 01-MAY-1998; 98US-00070844.

PR 01-MAY-1998; 98US-00070844.

XX (SCHM/) SCHMIDT R R.
XX (MILL/) MILLER P.

PI Schmidt RR, Miller P;

XX WPI; 2002-499691/53.

DR N-PSDB; ABK51025.

XX Transforming a plant with a polynucleotide encoding a polypeptide with
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
metabolism useful to increase yield and ammonium and osmotic stress
tolerance.

XX Claim 7; Page 27-28; 35pp; English.

XX The invention relates to a method of modulating nitrogen metabolism in
CC plant cells, comprising transcribing a plant cell with a polynucleotide
CC encoding a polypeptide having glutamate dehydrogenase activity, and
CC culturing the cell to produce descendant cells which express the
CC polypeptide. The method is used to provide plants with increased yield,
CC improved ammonium assimilation properties, increased tolerance to ammonia
CC toxicity, improved osmotic stress tolerance and improved composition. The
CC present sequence represents the amino acid sequence of Chlorella
CC sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in

26 1239.5 49.3 448 6 ABU29386 Protein e
27 1239.5 49.3 448 8 ADH97147 E. faecal
28 1239 49.3 449 5 AAU91467 Haemophil
29 1238 49.3 449 4 AAB88536 Haemophil
30 1238 49.3 449 6 ABU30172 Protein e
31 1236.5 49.2 449 5 ABP28423 Streptoco
32 1234.5 49.1 448 7 ADH85999 Enterococ
33 1230.5 49.0 449 6 ABU44405 Protein e
34 1230 48.9 449 6 ABU38946 Protein e
35 1221 48.6 448 8 ADK47974 Streptoco
36 1214 48.3 448 6 ABU46100 Protein e
37 1212 48.2 448 6 ABU01740 S. pneumo
38 1211.5 48.2 448 8 ADH97149 E. faecal
39 1210.5 48.2 458 8 ADS28251 Bacterial
40 1207.5 48.1 464 6 ABU23354 Protein e
41 1205.5 48.0 424 6 ADN17964 Bacterial
42 1205.5 48.0 444 6 ABU20518 Protein e
43 1204 47.9 447 2 AAW08092 Glutamina
44 1201 47.8 447 2 AAW60830 E. coli g
45 1201 47.8 447 6 ABU15360 Protein e

```

CC the method of the invention
XX
SQ Sequence 487 AA;

Query Match      100.0%; Score 2513; DB 5; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.6e-231;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPE 60
DB 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPE 60
QY 61 QOEFMQAVREAVASIQPVFEKRPPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGPRV 120
DB 61 QOEFMQAVREAVASIQPVFEKRPPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGPRV 120
QY 121 QYSSAIGPYKGLRPHPSVNLNLSIMKFLAFAQEIQFKNLSLTLPMMGGGKGSDFDPKGSDAE 180
DB 121 QYSSAIGPYKGLRPHPSVNLNLSIMKFLAFAQEIQFKNLSLTLPMMGGGKGSDFDPKGSDAE 180
QY 181 VMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGYLFQGYKRITKNTVGLTPKGQBYG 240
DB 181 VMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGYLFQGYKRITKNTVGLTPKGQBYG 240
QY 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAEELLEKGATVLSLS 300
DB 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAEELLEKGATVLSLS 300
QY 301 DSQGYVVEPNPFTREQLQAVQDMKKNNNSARISEYKSDTAVVGGRRKRPWELDCQVDIAF 360
DB 301 DSQGYVVEPNPFTREQLQAVQDMKKNNNSARISEYKSDTAVVGGRRKRPWELDCQVDIAF 360
QY 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAV 420
DB 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
QY 481 VKAQGAV 487
DB 481 VKAQGAV 487

RESULT 3
AAW15408
ID AAW15408 standard; protein; 512 AA.
XX

```

```

DR WPI; 2004-533134/51.
DR N-PSDB; ADQ36728.
XX
PT Increasing or decreasing nitrogen metabolism in plant cells, for plant
PT with increased yield and improved tolerance to ammonia toxicity and
PT osmotic stress, by transforming plant cell with nucleic acid having
PT glutamate dehydrogenase activity.
XX
PS Claim 7; SEQ ID NO 24; 36pp; English.
XX
CC The present invention relates to increasing or decreasing the nitrogen
CC metabolism in plant cells by transforming a plant cell with a
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
CC ADQ36731), or their fragments, which exhibits GDH activity. The
CC polynucleotide is operably linked to a polynucleotide encoding a
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
CC fragments that exhibit chloroplast transit activity. The method is useful
CC for increasing or decreasing the nitrogen metabolism in plant cells. The
CC methods, polynucleotides, and polypeptides are useful in producing plant
CC with increased yield, and with improved tolerance to ammonia toxicity,
CC osmotic stress, and composition of the crop or plant. The present
CC sequence is the mature alpha subunit of the NADP-specific GDH used in the
CC method of the invention.
XX
SQ Sequence 487 AA;

Query Match      100.0%; Score 2513; DB 8; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.6e-231;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPE 60
DB 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPE 60
QY 61 QOEFMQAVREAVASIQPVFEKRPPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGPRV 120
DB 61 QOEFMQAVREAVASIQPVFEKRPPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGPRV 120
QY 121 QYSSAIGPYKGLRPHPSVNLNLSIMKFLAFAQEIQFKNLSLTLPMMGGGKGSDFDPKGSDAE 180
DB 121 QYSSAIGPYKGLRPHPSVNLNLSIMKFLAFAQEIQFKNLSLTLPMMGGGKGSDFDPKGSDAE 180
QY 181 VMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGYLFQGYKRITKNTVGLTPKGQBYG 240
DB 181 VMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGYLFQGYKRITKNTVGLTPKGQBYG 240
QY 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAEELLEKGATVLSLS 300
DB 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAEELLEKGATVLSLS 300
QY 301 DSQGYVVEPNPFTREQLQAVQDMKKNNNSARISEYKSDTAVVGGRRKRPWELDCQVDIAF 360
DB 301 DSQGYVVEPNPFTREQLQAVQDMKKNNNSARISEYKSDTAVVGGRRKRPWELDCQVDIAF 360
QY 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAV 420
DB 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
QY 481 VKAQGAV 487
DB 481 VKAQGAV 487

RESULT 3
AAW15408
ID AAW15408 standard; protein; 512 AA.
XX

```

[illegible]

XX Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
 KW chloroplast; transgenic plant.
 XX
 OS Chlorella sorokiniana; strain UTEX 1230.
 XX
 PN WO9712983-Al.
 XX
 XX 10-APR-1997.
 XX
 XX 03-OCT-1996; 96WO-US015921.
 XX
 XX 06-OCT-1995; 95US-00541033.
 XX
 XX (UYFL) UNIV FLORIDA.
 XX
 XX Schmidt RR, Miller P;
 XX
 XX WPI; 1997-226226/20.
 XX
 XX N-PSDB; AAT64529, AAT64542.
 XX
 XX DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
 PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
 PT plant cells.
 XX
 XX Claim 1; Page 25-27; 61pp; English.
 XX
 XX 2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha
 CC (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-
 CC inducible, chloroplast-localised NADP-specific glutamate dehydrogenase
 CC (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha
 CC and beta subunits (see also AAW15411-12) that comprise the active NADP-
 CC GDH hexameric isoenzymes. The N metabolism of plants can be modulated
 CC (pref. increasing the assimilation of inorganic N into organic N) by
 CC transforming them with nucleotide sequences (see also AAT64529-30,
 CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
 CC proteins. Such plants show improved properties, e.g. increased crop yield
 CC and improved stress tolerance. Heterohexamers having alpha and beta
 CC subunits can be expressed that have heterohexamers having alpha and beta
 CC subunits can be expressed that have heterohexamers having alpha and beta
 CC ratios (i.e. higher capacity for glutamate synthesis) than homo-hexamers.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 XX Sequence 526 AA;
 SQ
 Query Match 99.8%; Score 2508; DB 2; Length 526;
 Best Local Similarity 100.0%; Pred. No. 1.9e-230; Indels 0; Gaps 0;
 Matches 486; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
 2 AVSLEEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGIRKPNPDRQLLTETPFMKDPEQ 61
 41 AVSLEEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGIRKPNPDRQLLTETPFMKDPEQ 100
 62 QEFMQAVREVAVSLQVPFKEKPELLPIFQIIVPEPVRITFRVSWLDDAGNLQVNRGRVQ 121
 101 QEFMQAVREVAVSLQVPFKEKPELLPIFQIIVPEPVRITFRVSWLDDAGNLQVNRGRVQ 160
 122 YSSALGPYKGLRHPNSVNLSTMKFLAFEQIFKNSITLTPMGGGKGGSDFPKGSDAEV 181
 161 YSSALGPYKGLRHPNSVNLSTMKFLAFEQIFKNSITLTPMGGGKGGSDFPKGSDAEV 220
 182 MRFCSQFMTELQHRHSYVDVPAGDIGVGARIGVLFQYKRITKNTYGLVLPKQGEYGG 241
 221 MRFCSQFMTELQHRHSYVDVPAGDIGVGARIGVLFQYKRITKNTYGLVLPKQGEYGG 280
 242 SEIRPEATGYGAVLFVENYLDKGSLSKRCRLVSGAGNVAQYCAELLEKGAIVLSLSD 301
 281 SEIRPEATGYGAVLFVENYLDKGSLSKRCRLVSGAGNVAQYCAELLEKGAIVLSLSD 340
 302 SQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 361
 341 SQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 400
 362 CATONEIDHDAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIITPCGAANAGGVAVS 421

Db 401 CATONEIDHDAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIITPCGAANAGGVAVS 460
 QY 422 GLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAMGPSRYNYDLAAGANIAGFTKVADAV 481
 Db 461 GLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAMGPSRYNYDLAAGANIAGFTKVADAV 520
 QY 482 KAQGAV 487
 Db 521 KAQGAV 526

RESULT 7
 AAU98950
 ID AAU98950 standard; protein; 526 AA.
 XX
 AC AAU98950;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE NADP-glutamate dehydrogenase alpha subunit.
 XX
 KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
 KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
 XX
 OS Chlorella sorokiniana.
 XX
 PN US2002062495-Al.
 XX
 XX 23-MAY-2002.
 XX
 XX 01-MAY-1998; 98US-00070844.
 PF
 XX 01-MAY-1998; 98US-00070844.
 PR
 XX (SCHM/) SCHMIDT R R.
 XX (MILL/) MILLER P.
 PA
 PI Schmidt RR, Miller P;
 XX
 XX WPI; 2002-499691/53.
 XX N-PSDB; ABK51007.
 XX
 XX Transforming a plant with a polynucleotide encoding a polypeptide with
 PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
 PT metabolism useful to increase yield and ammonium and osmotic stress
 PT tolerance.
 XX
 XX Claim 6; Page 13-15; 35pp; English.
 XX
 XX The invention relates to a method of modulating nitrogen metabolism in
 CC plant cells, comprising transforming a plant cell with a polynucleotide
 CC encoding a polypeptide having glutamate dehydrogenase activity, and
 CC culturing the cell to produce descendant cells which express the
 CC polypeptide. The method is used to provide plants with increased yield.
 CC improved ammonium assimilation properties, increased tolerance to ammonia
 CC toxicity, improved osmotic stress tolerance and improved composition. The
 CC present sequence represents the amino acid sequence of Chlorella
 CC sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the
 CC method of the invention
 XX
 XX Sequence 526 AA;
 SQ
 Query Match 99.8%; Score 2508; DB 5; Length 526;
 Best Local Similarity 100.0%; Pred. No. 1.9e-230; Indels 0; Gaps 0;
 Matches 486; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
 2 AVSLEEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGIRKPNPDRQLLTETPFMKDPEQ 61
 41 AVSLEEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGIRKPNPDRQLLTETPFMKDPEQ 100
 62 QEFMQAVREVAVSLQVPFKEKPELLPIFQIIVPEPVRITFRVSWLDDAGNLQVNRGRVQ 121
 101 QEFMQAVREVAVSLQVPFKEKPELLPIFQIIVPEPVRITFRVSWLDDAGNLQVNRGRVQ 160
 122 YSSALGPYKGLRHPNSVNLSTMKFLAFEQIFKNSITLTPMGGGKGGSDFPKGSDAEV 181
 161 YSSALGPYKGLRHPNSVNLSTMKFLAFEQIFKNSITLTPMGGGKGGSDFPKGSDAEV 220
 182 MRFCSQFMTELQHRHSYVDVPAGDIGVGARIGVLFQYKRITKNTYGLVLPKQGEYGG 241
 221 MRFCSQFMTELQHRHSYVDVPAGDIGVGARIGVLFQYKRITKNTYGLVLPKQGEYGG 280
 242 SEIRPEATGYGAVLFVENYLDKGSLSKRCRLVSGAGNVAQYCAELLEKGAIVLSLSD 301
 281 SEIRPEATGYGAVLFVENYLDKGSLSKRCRLVSGAGNVAQYCAELLEKGAIVLSLSD 340
 302 SQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 361
 341 SQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 400
 362 CATONEIDHDAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIITPCGAANAGGVAVS 421

Db 101 QEFMAQVREAVSLQPVPEKPELLPIPKQIVPEPVRITFRVSLDDAGNLQVNGFRVQ 160
Qy 122 YSSAIGPYKGLRPHPSVNLSTMKFLAPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEV 181
Db 161 YSSAIGPYKGLRPHPSVNLSTMKFLAPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEV 220
Qy 182 MRCQSPMTLQRLHISYVQDVPAGDIGVGAREIGVLFQYKRIITKNYTGVLTPKQEGVG 241
Db 221 MRCQSPMTLQRLHISYVQDVPAGDIGVGAREIGVLFQYKRIITKNYTGVLTPKQEGVG 280
Qy 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSD 301
Db 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSD 340
Qy 302 SQGYVEPENGFTRELQAVQDMKKNSARISEYKSDTAIVYVGGDRRKPWELDCQVDIAPP 361
Db 341 SQGYVEPENGFTRELQAVQDMKKNSARISEYKSDTAIVYVGGDRRKPWELDCQVDIAPP 400
Qy 362 CATONEIDEHDAELLIKHGCOYVVGAGNMPSTNEAIHKYNKAGIICPGKAANAGGVAVS 421
Db 401 CATONEIDEHDAELLIKHGCOYVVGAGNMPSTNEAIHKYNKAGIICPGKAANAGGVAVS 460
Qy 422 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
Db 461 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520
Qy 482 KAQAV 487
Db 521 KAQAV 526

RESULT 8
ID ADQ36707 standard; protein; 526 AA.
XX
AC ADQ36707;
DT 23-SEP-2004 (first entry)
XX
DE NADP-specific GDH alpha subunit precursor protein, SEQ ID 2.
XX
KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
XX
OS Chlorella sorokiniana.
XX
PN US2004128710-A1.
XX
PD 01-JUL-2004.
XX
PF 24-JUL-2003; 2003US-00627886.
XX
PR 01-MAY-1998; 98US-00070844.
XX
PA (SCHW/) SCHMIDT R R.
PA (MILL/) MILLER P.
XX
PI Schmidt RR, Miller P;
XX
XX WPI; 2004-533134/51.
DR N-PSDB; ADQ36706.
XX

Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
XX
PS Claim 7; SEQ ID NO 2; 36pp; English.
XX
CC The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase

CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, ADQ36731), or their fragments, which exhibits GDH activity. The polynucleotide is operably linked to a polynucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, osmotic stress, and composition of the crop or plant. The present sequence is the precursor protein of the alpha subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the invention.
XX
SQ Sequence 526 AA;

Query Match 99.8%; Score 2508; DB 8; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.9e-230;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AVSLEEQISAMDATTGDTALQKAVKQMATVAGTEGLVHGINKPDVROLLTEIFMKDPEQ 61
Db 41 AVSLEEQISAMDATTGDTALQKAVKQMATVAGTEGLVHGINKPDVROLLTEIFMKDPEQ 100
Qy 62 QEFMAQVREAVSLQPVPEKPELLPIPKQIVPEPVRITFRVSLDDAGNLQVNGFRVQ 121
Db 101 QEFMAQVREAVSLQPVPEKPELLPIPKQIVPEPVRITFRVSLDDAGNLQVNGFRVQ 160
Qy 122 YSSAIGPYKGLRPHPSVNLSTMKFLAPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEV 181
Db 161 YSSAIGPYKGLRPHPSVNLSTMKFLAPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEV 220
Qy 182 MRCQSPMTLQRLHISYVQDVPAGDIGVGAREIGVLFQYKRIITKNYTGVLTPKQEGVG 241
Db 221 MRCQSPMTLQRLHISYVQDVPAGDIGVGAREIGVLFQYKRIITKNYTGVLTPKQEGVG 280
Qy 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSD 301
Db 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSD 340
Qy 302 SQGYVEPENGFTRELQAVQDMKKNSARISEYKSDTAIVYVGGDRRKPWELDCQVDIAPP 361
Db 341 SQGYVEPENGFTRELQAVQDMKKNSARISEYKSDTAIVYVGGDRRKPWELDCQVDIAPP 400
Qy 362 CATONEIDEHDAELLIKHGCOYVVGAGNMPSTNEAIHKYNKAGIICPGKAANAGGVAVS 421
Db 401 CATONEIDEHDAELLIKHGCOYVVGAGNMPSTNEAIHKYNKAGIICPGKAANAGGVAVS 460
Qy 422 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
Db 461 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520
Qy 482 KAQAV 487
Db 521 KAQAV 526

RESULT 9
AAW15411
ID AAW15411 standard; protein; 487 AA.
XX
AC AAW15411;
XX
DT 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
DE NADP-specific glutamate dehydrogenase alpha subunit.
XX
KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW chloroplast; transgenic plant.
XX
OS Chlorella sorokiniana; strain UTEX 1230.
XX

```
PN WO9712983-A1.
XX
PD 10-APR-1997.
XX
PF 03-OCT-1996; 96WO-US015921.
XX
PR 06-OCT-1995; 95US-00541033.
XX
PA (UYFL ) UNIV FLORIDA.
XX
PI Schmidt RR, Miller P;
XX
DR WPI; 1997-226226/20.
DR N-PSDB; AAT64547.
XX
PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT plant cells.
XX
PS Claim 1; Page 44-46; 61pp; English.
XX
CC 2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature
CC alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an
CC ammonium-inducible, chloroplast-localised hexameric NADP-specific
CC glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
CC They are produced by removal of transit peptides from the precursor
CC proteins (AAW15407-08). The N metabolism of plants can be modulated
CC (pref. increasing the assimilation of inorganic N into organic N) by
CC transforming them with nucleotide sequences (see also AAT64529-30,
CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC proteins. Such plants show improved properties, e.g. increased crop yield
CC and improved stress tolerance. Heterohexamers having alpha and beta
CC subunits can be expressed that have higher aminating/deaminating activity
CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 487 AA;

Query Match 99.7%; Score 2505; DB 2; Length 487;
Best Local Similarity 99.8%; Pred. No. 3.3e-230;
Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLLETFMKDPE 60
DB 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLLETFMKDPE 60
QY 61 QOEFMQAVREVAVSLOPVEKEPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRV 120
DB 61 QOEFMQAVREVAVSLOPVEKEPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRV 120
QY 121 QYSSAIGPYKGLRPHPSVNLSTIMKFLAPEQIFKNSLTTLPMGGGKGSDPDKGSDAE 180
DB 121 QYSSAIGPYKGLRPHPSVNLSTIMKFLAPEQIFKNSLTTLPMGGGKGSDPDKGSDAE 180
QY 181 VNRFCQSFMTLQRIHSYVDVPAGDIGVAREIGYLFQYKRITKNTYGVLTTPKQGEYG 240
DB 181 VNRFCQSFMTLQRIHSYVDVPAGDIGVAREIGYLFQYKRITKNTYGVLTTPKQGEYG 240
QY 241 GSEIRPEATGYGAVLFVENVLDKESLKGKCLVSGAGNVAQYCAELLLEGAIVLSLS 300
DB 241 GSEIRPEATGYGAVLFVENVLDKESLKGKCLVSGAGNVAQYCAELLLEGAIVLSLS 300
QY 301 DSQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGGRRKFWELDCQVDIAF 360
DB 301 DSQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGGRRKFWELDCQVDIAF 360
QY 361 PCATQNEIDEHDAELLIKHGQCYVVEGANMPSTNEAIHKYNKAGIICYPGKAANAGGVAV 420
DB 361 PCATQNEIDEHDAELLIKHGQCYVVEGANMPSTNEAIHKYNKAGIICYPGKAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADA 480
DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADA 480

QY 481 VKAQGAV 487
DB 481 VKAQGAV 487

RESULT 10
AAW15412
ID AAW15412 standard; protein; 476 AA.
XX
AC AAW15412;
XX
DT 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
DE NADP-specific glutamate dehydrogenase beta subunit.
XX
KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW chloroplast; transgenic plant.
XX
OS Chlorella sorokiniana; strain UTEX 1230.
XX
PN WO9712983-A1.
XX
PD 10-APR-1997.
XX
PF 03-OCT-1996; 96WO-US015921.
XX
PR 06-OCT-1995; 95US-00541033.
XX
PA (UYFL ) UNIV FLORIDA.
XX
PI Schmidt RR, Miller P;
XX
DR WPI; 1997-226226/20.
DR N-PSDB; AAT64548.
XX
PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT plant cells.
XX
PS Claim 1; Page 48-50; 61pp; English.
XX
CC 2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature
CC alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an
CC ammonium-inducible, chloroplast-localised hexameric NADP-specific
CC glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
CC They are produced by removal of transit peptides from the precursor
CC proteins (AAW15407-08). The N metabolism of plants can be modulated
CC (pref. increasing the assimilation of inorganic N into organic N) by
CC transforming them with nucleotide sequences (see also AAT64529-30,
CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC proteins. Such plants show improved properties, e.g. increased crop yield
CC and improved stress tolerance. Heterohexamers having alpha and beta
CC subunits can be expressed that have higher aminating/deaminating activity
CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 476 AA;

Query Match 98.1%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.1e-226;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MDATTGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLLETFMKDPEQOEFMQAVREV 71
DB 1 MDATTGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLLETFMKDPEQOEFMQAVREV 60
QY 72 AVSLQPVPEKEPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRVYSSAIGPYKG 131
DB 61 AVSLQPVPEKEPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRVYSSAIGPYKG 120
QY 132 GLRPHPSVNLSTIMKFLAPEQIFKNSLTTLPMGGGKGSDPDKGSDAEVNRFCQSFMT 191
```

Db 121 GLRFHPSVNLIMKFLAPEQIFKNSLTTLPMGGKGGSDFDPKGSDAEVMEFQCSPFTE 180
 QY 192 LQRHSISYVDVPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKQGYGSSIRPEATGY 251
 Db 181 LQRHSISYVDVPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKQGYGSSIRPEATGY 240
 QY 252 GAVLFVENVLKDKGESLKGKCLVSGAGNVAQYCAELILLEKGAIVLSLSDSQGYVYEPNG 311
 Db 241 GAVLFVENVLKDKGESLKGKCLVSGAGNVAQYCAELILLEKGAIVLSLSDSQGYVYEPNG 300
 QY 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKPMWELDCQVDIAFPCCATQNEIDEH 371
 Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKPMWELDCQVDIAFPCCATQNEIDEH 360
 QY 372 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 431
 Db 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 420
 QY 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 487
 Db 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476

RESULT 11

AAU98955
 ID AAU98955 standard; protein; 476 AA.
 XX
 AC AAU98955;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Mature NADP-glutamate dehydrogenase beta subunit.
 XX
 KW NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
 KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
 XX
 OS Chlorella sorokiniana.

US2002062495-A1.

XX
 XX 23-MAY-2002.
 XX
 XX 01-MAY-1998; 98US-00070844.
 XX
 XX 01-MAY-1998; 98US-00070844.
 XX
 XX (SCHM/) SCHMIDT R R.
 XX (MILL/) MILLER P.
 XX
 XX Schmidt RR, Miller P;
 XX
 XX WPI; 2002-499691/53.
 XX N-PSDB; ABK51026.
 XX
 XX Transforming a plant with a polynucleotide encoding a polypeptide with
 PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
 PT metabolism useful to increase yield and ammonium and osmotic stress
 PT tolerance.
 XX
 XX Claim 7; Page 31-32; 35pp; English.
 XX
 CC The invention relates to a method of modulating nitrogen metabolism in
 CC plant cells, comprising transforming a plant cell with a polynucleotide
 CC encoding a polypeptide having glutamate dehydrogenase activity, and
 CC culturing the cell to produce descendant cells which express the
 CC polypeptide. The method is used to provide plants with increased yield,
 CC improved ammonium assimilation properties, increased tolerance to ammonia
 CC toxicity, improved osmotic stress tolerance and improved composition. The
 CC present sequence represents the amino acid sequence of Chlorella
 CC sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the
 CC method of the invention

XX SQ Sequence 476 AA;
 Query Match 98.1%; Score 2465; DB 5; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2.1e-226;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 MDATGGDTALQKAVKQMATKAGTEGLVHGKIKNDPVRQLLTEIFPKMQDEQEFMQAVREV 71
 Db 1 MDATGGDTALQKAVKQMATKAGTEGLVHGKIKNDPVRQLLTEIFPKMQDEQEFMQAVREV 60
 QY 72 AVSLQPVFEKPELLPIPKQIVPEPVRTTFVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
 Db 61 AVSLQPVFEKPELLPIPKQIVPEPVRTTFVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
 QY 132 GLRFHPSVNLIMKFLAPEQIFKNSLTTLPMGGKGGSDFDPKGSDAEVMEFQCSPFTE 191
 Db 121 GLRFHPSVNLIMKFLAPEQIFKNSLTTLPMGGKGGSDFDPKGSDAEVMEFQCSPFTE 180
 QY 192 LQRHSISYVDVPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKQGYGSSIRPEATGY 251
 Db 181 LQRHSISYVDVPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKQGYGSSIRPEATGY 240
 QY 252 GAVLFVENVLKDKGESLKGKCLVSGAGNVAQYCAELILLEKGAIVLSLSDSQGYVYEPNG 311
 Db 241 GAVLFVENVLKDKGESLKGKCLVSGAGNVAQYCAELILLEKGAIVLSLSDSQGYVYEPNG 300
 QY 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKPMWELDCQVDIAFPCCATQNEIDEH 371
 Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKPMWELDCQVDIAFPCCATQNEIDEH 360
 QY 372 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 431
 Db 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 420
 QY 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 487
 Db 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476

RESULT 12

ADQ36731
 ID ADQ36731 standard; protein; 476 AA.
 XX
 AC ADQ36731;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Mature NADP-specific GDH beta subunit, SEQ ID 26.
 XX
 KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
 KW beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
 XX
 OS Chlorella sorokiniana.
 XX
 XX US2004128710-A1.
 XX
 XX 01-JUL-2004.
 XX
 XX 24-JUL-2003; 2003US-00627886.
 XX
 XX 01-MAY-1998; 98US-00070844.
 XX
 XX (SCHM/) SCHMIDT R R.
 XX (MILL/) MILLER P.
 XX
 XX Schmidt RR, Miller P;
 XX
 XX WPI; 2004-533134/51.
 XX DR N-PSDB; ADQ36730.
 XX
 XX Increasing or decreasing nitrogen metabolism in plant cells, for plant
 PT with increased yield and improved tolerance to ammonia toxicity and

PT osmotic stress, by transforming plant cell with nucleic acid having
PT glutamate dehydrogenase activity.
XX
PS Claim 7; SEQ ID NO 26; 36pp; English.
XX
CC The present invention relates to increasing or decreasing the nitrogen
CC metabolism in plant cells by transforming a plant cell with a
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
CC ADQ36731), or their fragments, which exhibits GDH activity. The
CC polynucleotide is operably linked to a polynucleotide encoding a
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
CC fragments that exhibit chloroplast transit activity. The method is useful
CC for increasing or decreasing the nitrogen metabolism in plant cells. The
CC methods, polynucleotides, and polypeptides are useful in producing plant
CC with increased yield, and with improved tolerance to ammonia toxicity,
CC osmotic stress, and composition of the crop or plant. The present
CC sequence is the mature beta subunit of the NADP-specific GDH used in the
CC method of the invention.
XX
SQ Sequence 476 AA;

Query Match 98.1%; Score 2465; DB 8; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.1e-226; Mismatches 0; Indels 0; Gaps 0;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 MDATGDTALQKAVKQMATKAGTEGLVHGIKNPDPVRLTLTIFMKDPEQQFMAQVREV 71
DB 1 MDATGDTALQKAVKQMATKAGTEGLVHGIKNPDPVRLTLTIFMKDPEQQFMAQVREV 60
QY 72 AVSLQPVFKRPELLIPKQIVPEPVTIFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
DB 61 AVSLQPVFKRPELLIPKQIVPEPVTIFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
QY 132 GLRPHPSVNLSTMKFLAPFQIIFNSLTITLPMGGGKGSDFDPKGSDAEWMRFQCSFWTE 191
DB 121 GLRPHPSVNLSTMKFLAPFQIIFNSLTITLPMGGGKGSDFDPKGSDAEWMRFQCSFWTE 180
QY 192 LQRHSYVDVPAGDIGVAREIGVLFQYKRTKNYTGVLTPKQEGVSGSIRPEATGY 251
DB 181 LQRHSYVDVPAGDIGVAREIGVLFQYKRTKNYTGVLTPKQEGVSGSIRPEATGY 240
QY 252 GAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 311
DB 241 GAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 300
QY 312 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPEWELDCQVDIAPPATQNEIDEH 371
DB 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPEWELDCQVDIAPPATQNEIDEH 360
QY 372 DAELLIKHGCGVYVGGANMPSNEAIHKYNKAGIYCPCGANAGAVSVGLEMTQNRMS 431
DB 361 DAELLIKHGCGVYVGGANMPSNEAIHKYNKAGIYCPCGANAGAVSVGLEMTQNRMS 420
QY 432 LNTWTRVEDRDKLERIMKDIYDSAMGPSRRYNDLAAGANIAGFTKVDADVAKQAGAV 487
DB 421 LNTWTRVEDRDKLERIMKDIYDSAMGPSRRYNDLAAGANIAGFTKVDADVAKQAGAV 476

RESULT 13
ABU38763
ID ABU38763 standard; protein; 445 AA.
XX
AC ABU38763;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #24290.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Pseudomonas aeruginosa.

XX WO200277183-A2.
XX PD 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-P8DB; ACA42633.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 66687; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 445 AA;

Query Match 52.1%; Score 1309; DB 6; Length 445;
Best Local Similarity 59.2%; Pred. No. 7.7e-116; Mismatches 120; Indels 6; Gaps 4;
Matches 263; Conservative 55;
QY 47 VRLTLTIFMKDPQQEFMAQVREVAVSLQVFKRPELLP--IFKQIVPEPVTIFRV 104
DB 5 VDAFLERLKRDPDPQEPHQAVEVLSLWFLFLEAPHYLEAGIIEIVEFALLFRVP 64
QY 105 WLDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAPFQIIFNSLTITLPMGG 164
DB 65 WDDQGRVVRNVRGVQMSAIGPYKGLRPHPSVNLSTMKFLAPFQIIFNSLTITLPMGG 124

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OM protein - protein search, using sw model

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2104.671 Million cell updates/sec

Title: US-10-627-886-4

Perfect score: 2638

Sequence: 1 MOTALVAKPIVACAWRSK.....GANIAGFTKVADAVKQAGV 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2638	100.0	512	9 US-09-070-844-4	Sequence 4, Appli
2	2638	100.0	512	16 US-10-627-886-4	Sequence 4, Appli
3	2621	99.4	526	9 US-09-070-844-2	Sequence 2, Appli
4	2621	99.4	526	16 US-10-627-886-2	Sequence 2, Appli
5	2508	95.1	487	9 US-09-070-844-24	Sequence 24, Appl
6	2508	95.1	487	16 US-10-627-886-24	Sequence 24, Appl
7	2465	93.4	476	9 US-09-070-844-26	Sequence 26, Appl
8	2465	93.4	476	16 US-10-627-886-26	Sequence 26, Appl
9	1309	49.6	444	15 US-10-282-122A-66697	Sequence 6687, A
10	1300.5	49.3	444	18 US-10-988-943-43	Sequence 43, Appl
11	1297.5	49.2	444	15 US-10-282-122A-65129	Sequence 65129, A

12	1294.5	49.1	444	15 US-10-282-122A-66041	Sequence 66041, A
13	1294.5	49.1	444	15 US-10-275-026A-152	Sequence 152, App
14	1287.5	48.8	449	15 US-10-282-122A-67538	Sequence 67538, A
15	1281	48.6	445	15 US-10-369-493-13947	Sequence 13947, A
16	1259	47.7	454	15 US-10-369-493-9839	Sequence 9839, Ap
17	1257.5	47.7	462	15 US-10-282-122A-45200	Sequence 45200, A
18	1239.5	47.0	448	15 US-10-282-122A-57310	Sequence 57310, A
19	1239.5	47.0	448	18 US-10-953-901-338	Sequence 338, App
20	1238	46.9	449	14 US-10-260-877-90	Sequence 90, Appl
21	1238	46.9	449	15 US-10-282-122A-58096	Sequence 58096, A
22	1230.5	46.6	449	15 US-10-282-122A-72329	Sequence 72329, A
23	1230	46.6	449	15 US-10-282-122A-66870	Sequence 66870, A
24	1214	46.0	448	15 US-10-282-122A-74024	Sequence 74024, A
25	1212	45.9	448	17 US-10-472-928-2632	Sequence 2632, App
26	1211.5	45.9	448	18 US-10-953-901-340	Sequence 340, App
27	1210.5	45.9	458	15 US-10-369-493-17284	Sequence 17284, A
28	1207.5	45.8	464	15 US-10-282-122A-51278	Sequence 51278, A
29	1205.5	45.7	424	15 US-10-369-493-617	Sequence 617, App
30	1205.5	45.7	444	15 US-10-282-122A-48442	Sequence 48442, A
31	1201	45.5	447	15 US-10-369-493-859	Sequence 859, App
32	1201	45.5	447	15 US-10-282-122A-43284	Sequence 43284, A
33	1199	45.5	443	15 US-10-282-122A-52117	Sequence 52117, A
34	1196.5	45.4	456	15 US-10-425-114-72961	Sequence 72961, A
35	1195.5	45.3	438	15 US-10-369-493-8215	Sequence 8215, Ap
36	1194	45.3	438	15 US-10-282-122A-60243	Sequence 60243, A
37	1191	45.1	447	20 US-11-073-550-80	Sequence 80, Appl
38	1191	45.1	447	9 US-09-738-626-6982	Sequence 6982, Ap
39	1185	44.9	447	20 US-11-073-550-82	Sequence 82, Appl
40	1184	44.9	448	15 US-10-282-122A-53998	Sequence 53998, A
41	1182.5	44.8	447	15 US-10-282-122A-75593	Sequence 75593, A
42	1181	44.8	447	15 US-10-282-122A-60810	Sequence 60810, A
43	1180.5	44.7	458	15 US-10-369-493-295	Sequence 295, App
44	1180	44.7	447	15 US-10-282-122A-72769	Sequence 72769, A
45	1178	44.7	447		

ALIGNMENTS

RESULT 1
US-09-070-844-4
; Sequence 4, Application US/09070844
; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155

TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-070-844-4

Query Match 100.0%; Score 2638; DB 9; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.7e-228; Indels 0; Gaps 0;
Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEQISAMDATGDTALQKAVKQMATKAGT 60
DB 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEQISAMDATGDTALQKAVKQMATKAGT 60
QY 61 EGLVHGKINPDVRLTLTEIFMKDPQEQEPMQAVREAVSLQVPFVKRPPELLPIFKQIPEP 120
DB 61 EGLVHGKINPDVRLTLTEIFMKDPQEQEPMQAVREAVSLQVPFVKRPPELLPIFKQIPEP 120
QY 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFSQIPKN 180
DB 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFSQIPKN 180
QY 181 SLTTLPMGGKGGSDPDPKGSDAEVMRFQCSFMTLQRHISYVQDVDPAGDIGVGAREIG 240
DB 181 SLTTLPMGGKGGSDPDPKGSDAEVMRFQCSFMTLQRHISYVQDVDPAGDIGVGAREIG 240
QY 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILV 300
DB 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILV 300
QY 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVVEPNPFTREQLQAVQDMKKKNSARISEY 360
DB 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVVEPNPFTREQLQAVQDMKKKNSARISEY 360
QY 361 KSDTAVYVGGDRRKPMELDCQVDIAFPQATQNEIDHDAELLIKHGQYVVEGANPSTNE 420
DB 361 KSDTAVYVGGDRRKPMELDCQVDIAFPQATQNEIDHDAELLIKHGQYVVEGANPSTNE 420
QY 421 AIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTREVRDKLERIMKOIYDSAM 480
DB 421 AIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTREVRDKLERIMKOIYDSAM 480

RESULT 2
US-10-627-886-4
Sequence 4, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE -- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UP-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-627-886-4

Query Match 100.0%; Score 2638; DB 16; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.7e-228; Indels 0; Gaps 0;
Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEQISAMDATGDTALQKAVKQMATKAGT 60
DB 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEQISAMDATGDTALQKAVKQMATKAGT 60
QY 61 EGLVHGKINPDVRLTLTEIFMKDPQEQEPMQAVREAVSLQVPFVKRPPELLPIFKQIPEP 120
DB 61 EGLVHGKINPDVRLTLTEIFMKDPQEQEPMQAVREAVSLQVPFVKRPPELLPIFKQIPEP 120
QY 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFSQIPKN 180
DB 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFSQIPKN 180
QY 181 SLTTLPMGGKGGSDPDPKGSDAEVMRFQCSFMTLQRHISYVQDVDPAGDIGVGAREIG 240
DB 181 SLTTLPMGGKGGSDPDPKGSDAEVMRFQCSFMTLQRHISYVQDVDPAGDIGVGAREIG 240
QY 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILV 300
DB 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILV 300
QY 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVVEPNPFTREQLQAVQDMKKKNSARISEY 360
DB 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVVEPNPFTREQLQAVQDMKKKNSARISEY 360
QY 361 KSDTAVYVGGDRRKPMELDCQVDIAFPQATQNEIDHDAELLIKHGQYVVEGANPSTNE 420
DB 361 KSDTAVYVGGDRRKPMELDCQVDIAFPQATQNEIDHDAELLIKHGQYVVEGANPSTNE 420
QY 421 AIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTREVRDKLERIMKOIYDSAM 480
DB 421 AIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTREVRDKLERIMKOIYDSAM 480
QY 481 GPSRRYNDVLAAGANIAGFTKVVADAVKAGAV 512
DB 481 GPSRRYNDVLAAGANIAGFTKVVADAVKAGAV 512

RESULT 3
US-09-070-844-2
Sequence 2, Application US/09070844

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; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-070-844-2

Query Match 99.4%; Score 2621; DB 9; Length 526;
Best Local Similarity 97.3%; Pred. No. 9.4e-227;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTALVAKPIVA-----CAWVRSKRDVRAKAVSLERQISAMDATTGDTFA 46
DB 1 MOTALVAKPIVAAPLAARPCRLAPWPCAWVRSKRDVRAKAVSLERQISAMDATTGDTFA 60
QY 47 LOKAVKQMATKAGTEGLVHGINKNPVROLLEIFMKDPEQOEFMQAVREVAVSLQPVFEK 106
DB 61 LOKAVKQMATKAGTEGLVHGINKNPVROLLEIFMKDPEQOEFMQAVREVAVSLQPVFEK 120
QY 107 REPELLPIKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPHSVNL 166
DB 121 REPELLPIKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPHSVNL 180
QY 167 SIMKFLAFQIFKNSLTTLLPMGGKGGSDFPKGSDAEVMRQCQSFMTLQRHSIVQD 226
DB 181 SIMKFLAFQIFKNSLTTLLPMGGKGGSDFPKGSDAEVMRQCQSFMTLQRHSIVQD 240
QY 227 VPAGDIGVGAREIGYLFQGYKRTKNTYGTGLTPKGOYGGSEIRPEATGYGAVLFVENVL 286
DB 241 VPAGDIGVGAREIGYLFQGYKRTKNTYGTGLTPKGOYGGSEIRPEATGYGAVLFVENVL 300
QY 287 XDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ 346
DB 301 XDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ 360
QY 347 DMKKKNNSARISYKSDTAVYVGGDRKRWELDCQVDIAFPFCATQNEIDHDAELLIKHC 406
DB 361 DMKKKNNSARISYKSDTAVYVGGDRKRWELDCQVDIAFPFCATQNEIDHDAELLIKHC 420

; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; FILING DATE: 03-OCT-96
; FILING DATE: 06-OCT-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: UF-155CD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-10-627-886-2

Query Match 99.4%; Score 2621; DB 16; Length 526;
Best Local Similarity 97.3%; Pred. No. 9.4e-227;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTALVAKPIVA-----CAWVRSKRDVRAKAVSLERQISAMDATTGDTFA 46
DB 1 MOTALVAKPIVAAPLAARPCRLAPWPCAWVRSKRDVRAKAVSLERQISAMDATTGDTFA 60
QY 47 LOKAVKQMATKAGTEGLVHGINKNPVROLLEIFMKDPEQOEFMQAVREVAVSLQPVFEK 106
DB 61 LOKAVKQMATKAGTEGLVHGINKNPVROLLEIFMKDPEQOEFMQAVREVAVSLQPVFEK 120
QY 107 REPELLPIKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPHSVNL 166
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Db 121 REELLPIFKQIIEPERVITFRVSWLDDAGNLQVNRGFRVQVSSAIGPYKGLRFPSPVNL 180
Qy 167 SIMKFLAFEPQIPKNSLTLLPMGGGKGGSDPDKGSDAEVVRFCQSPMTLQRIHISYVQD 226
Db 181 SIMKFLAFEPQIPKNSLTLLPMGGGKGGSDPDKGSDAEVVRFCQSPMTLQRIHISYVQD 240
Qy 227 VPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKQEGGSGSIRPEATGYGAVLFVENVL 286
Db 241 VPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKQEGGSGSIRPEATGYGAVLFVENVL 300
Qy 287 KDKGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYVPEPNGFTREQLQAVQ 346
Db 301 KDKGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYVPEPNGFTREQLQAVQ 360
Qy 347 DMKKQNSARISEYKSDTAVYVGGDRRKPMWELDCQVDIAPPCCATQNEIDEHDAELLIKHGC 406
Db 361 DMKKQNSARISEYKSDTAVYVGGDRRKPMWELDCQVDIAPPCCATQNEIDEHDAELLIKHGC 420
Qy 407 QYVVEGANMPSNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNTWTREVRD 466
Db 421 QYVVEGANMPSNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNTWTREVRD 480
Qy 467 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGA 512
Db 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGA 526

RESULT 5

US-09-070-844-24
; Sequence 24, Application US/09070844
; Patent No. US20020082495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-24

Query Match 95.1%; Score 2508; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.3e-216;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 AVSLEBQISAMDATTTGDF TALQKAVKOMATKAGTEGLVHGINKNPDVROLITLTFPMKDPEQ 86
Db 2 AVSLEBQISAMDATTTGDF TALQKAVKOMATKAGTEGLVHGINKNPDVROLITLTFPMKDPEQ 61
Qy 87 QEFMQAVREAVASLOPVFEKRPPELLPIFKQIVPEPVRTTFRVSWLDDAGNLQVNRGFRVQ 146
Db 62 QEFMQAVREAVASLOPVFEKRPPELLPIFKQIVPEPVRTTFRVSWLDDAGNLQVNRGFRVQ 121
Qy 147 YSSAIGPYKGLRFPSPVNL SIMKFLAFEPQIPKNSLTLLPMGGGKGGSDPDKGSDAEV 206
Db 122 YSSAIGPYKGLRFPSPVNL SIMKFLAFEPQIPKNSLTLLPMGGGKGGSDPDKGSDAEV 181
Qy 207 MRFQCSFMTLQRIHISYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKQEGYGG 266
Db 182 MRFQCSFMTLQRIHISYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKQEGYGG 241
Qy 267 SEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLEKGAIVLSLSD 326
Db 242 SEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLEKGAIVLSLSD 301
Qy 327 SOGYVYVPEPNGFTREQLQAVQDMKKQNSARISEYKSDTAVYVGGDRRKPMWELDCQVDIAPP 386
Db 302 SOGYVYVPEPNGFTREQLQAVQDMKKQNSARISEYKSDTAVYVGGDRRKPMWELDCQVDIAPP 361
Qy 387 CATQNEIDEHDAELLIKHGCQYVVEGANMPSNEAIHKYNKAGIICPGKAANAGGAVV 446
Db 362 CATQNEIDEHDAELLIKHGCQYVVEGANMPSNEAIHKYNKAGIICPGKAANAGGAVV 421
Qy 447 GLEMTQNRMSLNTWTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 506
Db 422 GLEMTQNRMSLNTWTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
Qy 507 KAQGA 512
Db 482 KAQGA 487

RESULT 6
US-10-627-886-24
; Sequence 24, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; APPLICATION NUMBER: 08/725,596
; FILING DATE: 03-OCT-96

APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-627-886-24

Query Match 95.1%; Score 2508; DB 16; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.3e-216;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKNDVROLLEIFMKDPEQ 86
DB 2 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKNDVROLLEIFMKDPEQ 61
QY 87 QBFMQAVREVAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGFRVQ 146
DB 62 QBFMQAVREVAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGFRVQ 121
QY 147 YSSAIGPYKGLRFPSPVNLSTMKFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEV 206
DB 122 YSSAIGPYKGLRFPSPVNLSTMKFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEV 181
QY 207 MFPCQSFTELORHISYQDVDPAGDIGVAREIGVLFQYKRITKNYTGVLTPKQEGYCG 266
DB 182 MFPCQSFTELORHISYQDVDPAGDIGVAREIGVLFQYKRITKNYTGVLTPKQEGYCG 241
QY 267 SEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLEKGAI VLSLSD 326
DB 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLEKGAI VLSLSD 301
QY 327 SQGYVPEPGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPELDCQVDIAPP 386
DB 302 SQGYVPEPGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPELDCQVDIAPP 361
QY 387 CATONEIDHDAELLKHGCGQYVVEGANMPSTNEAIHKYNKAGI IYCPGKAANAGGVAVS 446
DB 362 CATONEIDHDAELLKHGCGQYVVEGANMPSTNEAIHKYNKAGI IYCPGKAANAGGVAVS 421
QY 447 GLEMTQNRMSLNTREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAV 506
DB 422 GLEMTQNRMSLNTREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAV 481
QY 507 KAQGAV 512
DB 482 KAQGAV 487

RESULT 7
US-09-070-844-26
Sequence 26, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-070-844-26

Query Match 93.4%; Score 2465; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 9e-213;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNDVROLLEIFMKDPEQBFMQAVREV 96
DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNDVROLLEIFMKDPEQBFMQAVREV 60
QY 97 AVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
DB 61 AVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
QY 157 GLRPHSPVNLSTMKFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEVNRFCSFMTE 216
DB 121 GLRPHSPVNLSTMKFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEVNRFCSFMTE 180
QY 217 LQRHISYQDVDPAGDIGVAREIGVLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGY 276
DB 181 LQRHISYQDVDPAGDIGVAREIGVLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGY 240
QY 277 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLEKGAI VLSLSDSQGYVPENG 336
DB 241 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLEKGAI VLSLSDSQGYVPENG 300
QY 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPELDCQVDIAPPATONEIDEH 396
DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPELDCQVDIAPPATONEIDEH 360
QY 397 DAELLKHGCGQYVVEGANMPSTNEAIHKYNKAGI IYCPGKAANAGGVAVSGLMTQNRMS 456
DB 361 DAELLKHGCGQYVVEGANMPSTNEAIHKYNKAGI IYCPGKAANAGGVAVSGLMTQNRMS 420
QY 457 LNTTREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 512
DB 421 LNTTREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

RESULT 8
US-10-627-886-26
Sequence 26, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:

Db 125 GKGSGDFDPKGSKDAEVMRFQCSFMSBLYRHVHCADLDVPAGDIGVGAREIGYLFQYKRL 184
 QY 250 TKNYTGVLTPKQGEYCGSEIRPEATGYGAVLFVENVLKDKGESLKGKRLCVSGAGNVAQY 309
 Db 185 SNQFTSVLTGKGLSYGSLIRPEATGCGYVFAQEMLKDRGRGFCQORVAISGSGNVAQY 244
 QY 310 CAELLLKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAIVYG 369
 Db 245 AARKVMEMGGKVISLSDSGTLVAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLOFL 303
 QY 370 DRKPKWELDCOVDFIAPFCATQNEIDHDAELLIKHGCQVYVEGANMPSTNEAIHKYNKAG 429
 Db 304 EGRPPWGLAC--DIALPCATQNELDAEDARRLLANGCVCVAEGANMPSTLEAVDLFLEAG 361
 QY 430 IYPCGKAANAGGAVAVSGLEMTQNRMSLNWTRREVRDKLERIMKOIYDSA-MGPSRRYNN 488
 Db 362 ILYAPKASNAGGAVAVSGLEMSQAMRLRWSEGEVDTKLHGIMQSIHHACLLYGBEQGRV 421
 QY 489 DLAAGANIAGFTKVADAVAKQAV 512
 Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

RESULT 10

US-10-988-943-43
 ; Sequence 43, Application US/10988943
 ; Publication No. US20050176085A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Center for Genetic Engineering and Biotechnology
 ; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
 ; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
 ; TITLE OF INVENTION: COMPLEX MIXTURES.
 ; FILE REFERENCE: Proteomics CU2003-269
 ; CURRENT APPLICATION NUMBER: US/10/988,943
 ; CURRENT FILING DATE: 2004-11-15
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 43
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis (group B)
 US-10-988-943-43

Query Match 49.3%; Score 1300.5; DB 18; Length 444;
 Best Local Similarity 57.4%; Pred. No. 5.8e-108;
 Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 71 DVROLLTEIFMKDPEQBFMAQVREAVASLOPVFEKRPPELL--PIPKQIVEPERVITPRV 128
 Db 3 DLNTLPANLKQRPNQEPFHQAVEEVFMSLDPPFLAKNPKYQOSLLERIVEPERVVMFRV 62
 QY 129 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGGIRPHSPVNSIMKFLAFEQIFKNSLTLLPMG 188
 Db 63 TWQDDKGVQVNRGVYQVMSAIGPYKGGIRPHSPVNSIMKFLAFEQIFKNSLTLLPMG 122
 QY 189 GKGSGDFDPKGSKDAEVMRFQCSFMTQLQRHISYVQDVPAGDIGVGAREIGYLFQYK 248
 Db 123 GKGSGDFDPKGSKDAEVMRFQCSFMTQLQRHISYVQDVPAGDIGVGAREIGYLFQYK 182
 QY 249 ITKNYTGVLTPKQGEYCGSEIRPEATGYGAVLFVENVLKDKGESLKGKRLCVSGAGNVAQ 308
 Db 183 IRNEFSVLTGKLEWGGSLIRPEATGYGCVVFAQAMLQTRNDSFEGKRVLSGSGNVAQ 242
 QY 309 YCAELLLEKGAIVLSLSDSQGYVYEP-NGFTREQLQAVQDMKKNSARISEYKSDTAYV 367
 Db 243 YAAEKAIQIGAKVLTVSDSNGFVLPDPSGMTEQAALIELVEVRRE-KVATYAKEQGIQ 301
 QY 368 VDRRKPWELDCQVDIAFPATQNEIDHDAELLIKHGCQVYVEGANMPSTNEAIHKYNK 427
 Db 302 YFEKQKPGV--AAETALPCATQNELDEEAATLLANGCVCVAEGANMPSTLGAVEQFTK 359
 QY 428 AGIYPCGKAANAGGAVAVSGLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAMGPSRRY- 486

Db 360 AGILYAPKASNAGGAVATSGLEMSQNAIRLSWTRBEVDQRLFGIMQSIHESCL----KYG 415
 QY 487 ----NVDLAAGANIAGFTKVADAVAKQ 510
 Db 416 KVGDTVNVYNGANIAGFVKVADAMLAQ 443
 RESULT 11
 US-10-282-122A-65129
 ; Sequence 65129, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 65129
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-282-122A-65129

Query Match 49.2%; Score 1297.5; DB 15; Length 444;
 Best Local Similarity 57.4%; Pred. No. 1.1e-107;
 Matches 257; Conservative 70; Mismatches 106; Indels 15; Gaps 6;

QY 71 DVROLLTEIFMKDPEQBFMAQVREAVASLOPVFEKRPPELL--PIPKQIVEPERVITPRV 128
 Db 3 DLNTLPANLKQRPNQEPFHQAVEEVFMSLDPPFLAKNPKYQOSLLERIVEPERVVMFRV 62
 QY 129 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGGIRPHSPVNSIMKFLAFEQIFKNSLTLLPMG 188
 Db 63 TWQDDKGVQVNRGVYQVMSAIGPYKGGIRPHSPVNSIMKFLAFEQIFKNSLTLLPMG 122
 QY 189 GKGSGDFDPKGSKDAEVMRFQCSFMTQLQRHISYVQDVPAGDIGVGAREIGYLFQYK 248
 Db 123 GKGSGDFDPKGSKDAEVMRFQCSFMTQLQRHISYVQDVPAGDIGVGAREIGYLFQYK 182

Db 125 GKGSDFDPKGSDAEVMRFCQAFMSLYRHHIGADVDPAGDIGVGAREIGFLFGQYKRL 184

QY 250 TKNYTCVLTPKQOEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQY 309

Db 185 SNQFTSVLTGKGMTYGGSLIRPEATGFCGVFAEEMLKRRREQVEGKRVAISGSGNVAQY 244

QY 310 CAELLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVG 369

Db 245 AARKVMDLGGKVISLSDBEGTLYCEAGLSEEQWLALLELKNVKR-GRISELASAFGLEFR 303

QY 370 DRKPKWELDCQVDIAPPQATONEIDEHDAELLIKHCQYVVEGAMPSPTNEAIHKYNKAG 429

Db 304 AGQLFWSLPC--DIALPCATQNELDAESARTLLRNGCVCVAEGANWPTTLEAVDIFIEAG 361

QY 430 IYCFGKAANAGGAVSGLEMTQNMSLNWTREYVRDKLERIMKDIYDSAMG-PSRRYNV 488

Db 362 ILFAPGKASNAGGAVSGLEMSQNAWRLIWTGGEVDSKLHGIMQSIHHACVHYGENGRI 421

QY 489 DLAAGANIAGFTKVADAVKAQAV 512

Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

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Job time : 97.8047 secs

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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:01:27 ; Search time 27.4224 Seconds
(without alignments)
1393.764 Million cell updates/sec

Title: US-10-627-886-4
Perfect score: 2638
Sequence: 1 MOTALVAKPIVACAWRSRAK.....GANIAGFTKVDVAKQAGAV 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2638	100.0	512	US-08-541-033A-4	Sequence 4, Appli
2	2638	100.0	512	US-08-828-451-4	Sequence 4, Appli
3	2621	99.4	526	US-08-541-033A-2	Sequence 2, Appli
4	2621	99.4	526	US-08-828-451-2	Sequence 2, Appli
5	2508	95.1	487	US-08-541-033A-24	Sequence 24, Appli
6	2508	95.1	487	US-08-828-451-24	Sequence 24, Appli
7	2465	93.4	476	US-08-541-033A-26	Sequence 26, Appli
8	2465	93.4	476	US-08-828-451-26	Sequence 26, Appli
9	1309	49.6	450	US-09-328-352-5725	Sequence 26, Appli
10	1257.5	47.7	467	US-09-252-991A-20646	Sequence 5725, Ap
11	1234.5	46.8	448	US-09-134-000C-3884	Sequence 3884, Ap
12	1221	46.3	448	US-09-583-110-4489	Sequence 4489, Ap
13	1201	45.5	447	US-08-886-640-3	Sequence 3, Appli
14	1201	45.5	447	US-08-884-235-11	Sequence 11, Appli
15	1200	45.5	447	US-08-370-193A-11	Sequence 11, Appli
16	1191	45.1	452	US-09-489-039A-7937	Sequence 7937, Ap
17	1177.5	44.6	446	US-09-543-681A-6657	Sequence 6657, Ap
18	1177	44.6	447	US-08-508-761B-6	Sequence 6, Appli
19	1147	43.5	461	US-09-171-337A-5	Sequence 5, Appli
20	1147	43.5	461	US-09-631-022-5	Sequence 5, Appli
21	1143	43.3	449	US-08-831-753-1	Sequence 1, Appli
22	1037.5	39.3	454	US-09-538-092-767	Sequence 767, App
23	1012	38.4	368	US-09-107-433-4041	Sequence 4041, Ap
24	788.5	29.9	298	US-09-248-796A-17483	Sequence 17483, A
25	552.5	20.9	420	US-09-134-001C-3103	Sequence 3103, Ap
26	537.5	20.4	374	US-09-710-279-2162	Sequence 2162, Ap
27	537	20.4	509	US-09-902-540-11352	Sequence 11352, A

28 519 19.7 420 3 US-09-239-303-9 Sequence 9, Appli
29 482.5 18.3 409 4 US-09-902-540-12638 Sequence 12638, A
30 476.5 18.1 421 3 US-09-239-303-2 Sequence 2, Appli
31 458.5 17.4 427 4 US-09-328-352-6130 Sequence 6130, Ap
32 441 16.7 432 4 US-09-489-039A-13935 Sequence 13935, A
33 385 14.6 87 2 US-08-461-990B-22 Sequence 22, Appli
34 368 13.9 87 2 US-08-461-990B-20 Sequence 20, Appli
35 364.5 13.8 558 4 US-09-538-092-1153 Sequence 1153, Ap
36 357 13.5 87 2 US-08-461-990B-23 Sequence 23, Appli
37 357 13.5 558 4 US-09-538-092-832 Sequence 832, App
38 357 13.5 575 4 US-09-949-016-7622 Sequence 7622, Ap
39 357 13.5 575 4 US-09-248-796A-17482 Sequence 7623, Ap
40 346 13.1 176 4 US-09-949-016-7623 Sequence 7623, Ap
41 168 6.4 87 2 US-08-461-990B-21 Sequence 21, Appli
42 157.5 6.0 366 2 US-08-804-699-2 Sequence 2, Appli
43 139.5 5.3 356 2 US-08-461-990B-2 Sequence 2, Appli
44 138 5.2 1092 4 US-09-538-092-122 Sequence 122, App
45 131 5.0 351 4 US-09-198-452A-991 Sequence 991, App

ALIGNMENTS

RESULT 1

US-08-541-033A-4
; Sequence 4, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541.033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-541-033A-4

Query Match 100.0%; Score 2638; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 5.7e-235;
Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVACAWRSRAKDVRAKAVLSLEQISAMDATGDFTLQAKVQMATKAGT 60
DB 1 MOTALVAKPIVACAWRSRAKDVRAKAVLSLEQISAMDATGDFTLQAKVQMATKAGT 60

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QY 61 EGLVHGINKPDRVQLLTETFMKDPQEQFMAQVAVSLQVPRKRPPELLPIPKQIYEP 120
Db 61 EGLVHGINKPDRVQLLTETFMKDPQEQFMAQVAVSLQVPRKRPPELLPIPKQIYEP 120
QY 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFQIIPKN 180
Db 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFQIIPKN 180
QY 181 SLTTLPMGGGKGGSDFPDKGSDAEVMRFCQSPMTLQRHISYVQDVPAGDIGVGAREIG 240
Db 181 SLTTLPMGGGKGGSDFPDKGSDAEVMRFCQSPMTLQRHISYVQDVPAGDIGVGAREIG 240
QY 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLV 300
Db 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLV 300
QY 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKNNNSARISEY 360
Db 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKNNNSARISEY 360
QY 361 KSDTAVYVGDRRKPEWELDCQVDIAFPCCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNE 420
Db 361 KSDTAVYVGDRRKPEWELDCQVDIAFPCCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNE 420
QY 421 AIHKYNKAGIICPCGAANAGGAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM 480
Db 421 AIHKYNKAGIICPCGAANAGGAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM 480
QY 481 GPSRRYNDLAAGANIAGFTKVAADVAKQAGAV 512
Db 481 GPSRRYNDLAAGANIAGFTKVAADVAKQAGAV 512
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RESULT 2

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US-08-828-451-4
; Sequence 4, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UP155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-4
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Query Match 100.0%; Score 2638; DB 2; Length 512;

Best Local Similarity 100.0%; Pred. No. 5.7e-235; Indels 0; Gaps 0;

Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MOTALVAKPIVACAWRSASAKRDVRKAVSLSEEQISAMDATTTGDTALQKAVKQMATKAGT 60
QY 61 EGLVHGINKPDRVQLLTETFMKDPQEQFMAQVAVSLQVPRKRPPELLPIPKQIYEP 120
Db 61 EGLVHGINKPDRVQLLTETFMKDPQEQFMAQVAVSLQVPRKRPPELLPIPKQIYEP 120
QY 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFQIIPKN 180
Db 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFQIIPKN 180
QY 181 SLTTLPMGGGKGGSDFPDKGSDAEVMRFCQSPMTLQRHISYVQDVPAGDIGVGAREIG 240
Db 181 SLTTLPMGGGKGGSDFPDKGSDAEVMRFCQSPMTLQRHISYVQDVPAGDIGVGAREIG 240
QY 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLV 300
Db 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLV 300
QY 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKNNNSARISEY 360
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QY 361 KSDTAVYVGDRRKPEWELDCQVDIAFPCCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNE 420
Db 361 KSDTAVYVGDRRKPEWELDCQVDIAFPCCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNE 420
QY 421 AIHKYNKAGIICPCGAANAGGAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM 480
Db 421 AIHKYNKAGIICPCGAANAGGAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM 480
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Db 481 GPSRRYNDLAAGANIAGFTKVAADVAKQAGAV 512
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RESULT 3

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US-08-541-033A-2
; Sequence 2, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UP155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-541-033A-2

Query Match 99.4%; Score 2621; DB 2; Length 526;
Best Local Similarity 97.3%; Pred. No. 2.2e-233;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

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Db 1 MOTALVAKPIVAAPLAARPRCLAPWPCAWVRSKRDVRAKAVSLEEQISAMDATTTGDFTA 60
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QY 107 RPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFHPSVNL 166
Db 121 RPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFHPSVNL 180
QY 167 SIMKFLAFAQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSQFMTLQRHISYVQD 226
Db 181 SIMKFLAFAQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSQFMTLQRHISYVQD 240
QY 227 VPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVL 286
Db 241 VPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVL 300
QY 287 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQYVYEPNGFTREQLQAVQ 346
Db 301 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQYVYEPNGFTREQLQAVQ 360
QY 347 DMKKKNSARISYKSDTAVYVGDRLKPELDCQVDIAFPCCATQNEIDEHDAELLIKHGC 406
Db 361 DMKKKNSARISYKSDTAVYVGDRLKPELDCQVDIAFPCCATQNEIDEHDAELLIKHGC 420
QY 407 QYVVEGANPSTNEAITHKNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRD 466
Db 421 QYVVEGANPSTNEAITHKNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRD 480
QY 467 KLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADAVKAQGV 512
Db 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADAVKAQGV 526
```

RESULT 4

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US-08-828-451-2
; Sequence 2, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
```

```
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UP155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-451-2
```

```
Query Match 99.4%; Score 2621; DB 2; Length 526;
Best Local Similarity 97.3%; Pred. No. 2.2e-233;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
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QY 1 MOTALVAKPIVA-----CAWVRSKRDVRAKAVSLEEQISAMDATTTGDFTA 46
Db 1 MOTALVAKPIVAAPLAARPRCLAPWPCAWVRSKRDVRAKAVSLEEQISAMDATTTGDFTA 60
QY 47 LQKAVKOMATKAGTEGLVHGKIKNPVDRQLLTETFMKDPQEQEFMQAVREVAVSLQPVFEK 106
Db 61 LQKAVKOMATKAGTEGLVHGKIKNPVDRQLLTETFMKDPQEQEFMQAVREVAVSLQPVFEK 120
QY 107 RPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFHPSVNL 166
Db 121 RPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFHPSVNL 180
QY 167 SIMKFLAFAQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSQFMTLQRHISYVQD 226
Db 181 SIMKFLAFAQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSQFMTLQRHISYVQD 240
QY 227 VPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVL 286
Db 241 VPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVL 300
QY 287 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQYVYEPNGFTREQLQAVQ 346
Db 301 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQYVYEPNGFTREQLQAVQ 360
QY 347 DMKKKNSARISYKSDTAVYVGDRLKPELDCQVDIAFPCCATQNEIDEHDAELLIKHGC 406
Db 361 DMKKKNSARISYKSDTAVYVGDRLKPELDCQVDIAFPCCATQNEIDEHDAELLIKHGC 420
QY 407 QYVVEGANPSTNEAITHKNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRD 466
Db 421 QYVVEGANPSTNEAITHKNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRD 480
QY 467 KLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADAVKAQGV 512
Db 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADAVKAQGV 526
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RESULT 5

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US-08-541-033A-24
; Sequence 24, Application US/08541033A
; Patent No. 5879941
```

GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-541-033A-24

Query Match 95.1%; Score 2508; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.4e-223;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AVSLEEQISAMDATGDFALQKAVKQATKAGTEGLVHGINKPDPVROLLEIFMKDPEQ 86
DB 2 AVSLEEQISAMDATGDFALQKAVKQATKAGTEGLVHGINKPDPVROLLEIFMKDPEQ 61

QY 87 QEFMQAVREAVSLQPVPEKPELLPIPKQIVPEPVRTVFRVSWLDDAGNLQVNRGFRVQ 146
DB 62 QEFMQAVREAVSLQPVPEKPELLPIPKQIVPEPVRTVFRVSWLDDAGNLQVNRGFRVQ 121

QY 147 YSSAIGPYKGLRPHPSVNLTKMLFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEV 206
DB 122 YSSAIGPYKGLRPHPSVNLTKMLFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEV 181

QY 207 MRFCSFMTLQRLHSYVDVDPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGYGG 266
DB 182 MRFCSFMTLQRLHSYVDVDPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGYGG 241

QY 267 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSD 326
DB 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSD 301

QY 327 SQGYVEPNFTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPMELDCQVDIAPP 386
DB 302 SQGYVEPNFTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPMELDCQVDIAPP 361

QY 387 CATONEIDBDHDAELIKHGCQVYVVGANMPSNEAIHKYNKAGIICPGKAANAGGAVS 446
DB 362 CATONEIDBDHDAELIKHGCQVYVVGANMPSNEAIHKYNKAGIICPGKAANAGGAVS 421

QY 447 GLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGPSRRYNYDLAAGANIAGFTTKVADAV 506
DB 422 GLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGPSRRYNYDLAAGANIAGFTTKVADAV 481

QY 507 KAQNAV 512
DB 482 KAQNAV 487

RESULT 6
US-08-828-451-24
Sequence 24, Application US/08828451
Patent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-451-24

Query Match 95.1%; Score 2508; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.4e-223;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AVSLEEQISAMDATGDFALQKAVKQATKAGTEGLVHGINKPDPVROLLEIFMKDPEQ 86
DB 2 AVSLEEQISAMDATGDFALQKAVKQATKAGTEGLVHGINKPDPVROLLEIFMKDPEQ 61

QY 87 QEFMQAVREAVSLQPVPEKPELLPIPKQIVPEPVRTVFRVSWLDDAGNLQVNRGFRVQ 146
DB 62 QEFMQAVREAVSLQPVPEKPELLPIPKQIVPEPVRTVFRVSWLDDAGNLQVNRGFRVQ 121

QY 147 YSSAIGPYKGLRPHPSVNLTKMLFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEV 206
DB 122 YSSAIGPYKGLRPHPSVNLTKMLFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEV 181

QY 207 MRFCSFMTLQRLHSYVDVDPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGYGG 266
DB 182 MRFCSFMTLQRLHSYVDVDPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGYGG 241

QY 267 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSD 326
DB 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSD 301

Db 242 SEIRPEATGYGAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSD 301
QY 327 SQCYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFP 386
Db 302 SQCYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFP 361
QY 387 CATONEIDEHDAELLKHGCOYVVEGANPSTNEAIHKYNKAGIICRCGKAANAGVAVS 446
Db 362 CATONEIDEHDAELLKHGCOYVVEGANPSTNEAIHKYNKAGIICRCGKAANAGVAVS 421
QY 447 GLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGFSRRYVNDLAAGANIAGFTKVVADAV 506
Db 422 GLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGFSRRYVNDLAAGANIAGFTKVVADAV 481
QY 507 KAQAV 512
Db 482 KAQAV 487

RESULT 7

US-08-541-033A-26
; Sequence 26, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-541-033A-26

Query Match 93.4%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.9e-219;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 MDATTGDTALQKAVQKMATKAGTEGLVHGKINPDRQLLTETFMKDPQEQBFMAQVREV 96
Db 1 MDATTGDTALQKAVQKMATKAGTEGLVHGKINPDRQLLTETFMKDPQEQBFMAQVREV 60
QY 97 AVSLQPVPEKRPPELLPIKQIIVEPERVITFRVSWLDDAGNLQVNRGFRVOYSSATGPYKG 156
Db 61 AVSLQPVPEKRPPELLPIKQIIVEPERVITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKG 120

QY 157 GLRPHPSVNLSTMKFLAPEQIFKNLSLTLLPMGGGKGGSDFDPKGKSDAEVMMFQCSFMTE 216
Db 121 GLRPHPSVNLSTMKFLAPEQIFKNLSLTLLPMGGGKGGSDFDPKGKSDAEVMMFQCSFMTE 180
QY 217 LORHLSYVQDVDPAGDIGVAREIGYLFQYKRTKNYTGVLTPKGOEYGSGSIRPEATGY 276
Db 181 LORHLSYVQDVDPAGDIGVAREIGYLFQYKRTKNYTGVLTPKGOEYGSGSIRPEATGY 240
QY 277 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNG 336
Db 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNG 300
QY 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFPQATONEIDEH 396
Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKRWELDCQVDIAFPQATONEIDEH 360
QY 397 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIICRCGKAANAGVAVSGLGMTQNRMS 456
Db 361 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIICRCGKAANAGVAVSGLGMTQNRMS 420
QY 457 LNWTRREEVRDKLERIMKDIYDSAMGFSRRYVNDLAAGANIAGFTTKVADAVKAQAV 512
Db 421 LNWTRREEVRDKLERIMKDIYDSAMGFSRRYVNDLAAGANIAGFTTKVADAVKAQAV 476

RESULT 8

US-08-828-451-26
; Sequence 26, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-451-26

Query Match 93.4%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.9e-219;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 37 MDATTGDTALOKAVQKATKAGTGLVHGIKNPDVROLTLTEIFMKDPEQEFMQAVREV 96
Db 1 MDATTGDTALOKAVQKATKAGTGLVHGIKNPDVROLTLTEIFMKDPEQEFMQAVREV 60
QY 97 AVSLQPVFEKRPPELLPIPKQIIVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
Db 61 AVSLQPVFEKRPPELLPIPKQIIVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
QY 157 GLRFPSPVNLSTMKFLAEPQIFKNSLTTLPMGGGKGSDPDPKGSDAEVRMPCOSPMTE 216
Db 121 GLRFPSPVNLSTMKFLAEPQIFKNSLTTLPMGGGKGSDPDPKGSDAEVRMPCOSPMTE 180
QY 217 LQRHLSYVDVPAGDIGVAREIGVLFQYKRITKNYTGVLTPKGOEYGGSEIRPEATGY 276
Db 181 LQRHLSYVDVPAGDIGVAREIGVLFQYKRITKNYTGVLTPKGOEYGGSEIRPEATGY 240
QY 277 GAVLFVENVLDKGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 336
Db 241 GAVLFVENVLDKGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 300
QY 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 396
Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360
QY 397 DAELLLKHGCGVYVVGANMPSTNEAIHKYNKAGIICPGKAAAGGAVSGLMNTQNRMS 456
Db 361 DAELLLKHGCGVYVVGANMPSTNEAIHKYNKAGIICPGKAAAGGAVSGLMNTQNRMS 420
QY 457 LNWTRREVRDKLERIMKDIYDSAMPSSRRYVVDLAAGANIAGFTKVADAVKAQGV 512
Db 421 LNWTRREVRDKLERIMKDIYDSAMPSSRRYVVDLAAGANIAGFTKVADAVKAQGV 476
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RESULT 9

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US-09-252-991A-20646
; Sequence 20646, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20646
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20646
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Query Match 49.6%; Score 1309; DB 4; Length 450;
Best Local Similarity 59.2%; Pred. No. 3e-112;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 72 VROLTLTEIFMKDPEQEFMQAVREVAVSLQPVFEKRPPELLP--IFKQIIVEPVRVITFRVS 129
Db 10 VDAFLERLKRDPDQEFHQAVEEVLRSLWPPLEANPHYLEAGIIEIVPERAILFRVP 69
QY 130 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAEPQIFKNSLTTLPMGG 189
Db 70 WYDDQGRVRNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAEPQIFKNSLTTLPMGG 129
QY 190 KGKGSDFDPKGSDAEVRMPCOSFMTLORHISYVQDVDPAGDIGVAREIGVLFQYKRI 249
Db 130 KGKGSDFDPKGSDAEVRMPCOSFMTLORHISYVQDVDPAGDIGVAREIGVLFQYKRL 189
QY 250 TKNYTGVLTPKGOEYGGSEIRPEATGYGAVLFVENVLDKGESLKGKRCVSGAGNVAQY 309
```

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Db 190 SNQFTSVLTGKGLSYGSLTRPEATGFCVYFAQEMLKDRGRGPDGQVRVAISGSGNVAQY 249
QY 310 CAELLLKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVYG 369
Db 250 AARKVMEGKGKVISLSLSDSEGTLYAEAGLSDBQEWYLMELKNVRR-GRIREMAEQFSLQFL 308
QY 370 DRRKPWELDCQVDIAFPCCATQNEIDEHDAELLLKHGCGVYVVGANMPSTNEAIHKYNKAG 429
Db 309 EGRRPWGLAC--DIALPCATQNEIDAEARLLANGCVCVABGANMPSTLEAVDLFLBAG 366
QY 430 ILYCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGPSRRYVY 488
Db 367 ILYAPGKASNAGGAVVSGLEMSQNAMLRMWSEGEVDYKLHGIMQSIHACILLYGEEQORV 426
QY 489 DLAAGANIAGFTKVADAVKAQGV 512
Db 427 NYVKGANIAGFVKVADAVKAQGV 450

RESULT 10
US-09-328-352-5725
; Sequence 5725, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5725
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5725
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Query Match 47.7%; Score 1257.5; DB 4; Length 467;
Best Local Similarity 55.9%; Pred. No. 1.9e-107;
Matches 256; Conservative 61; Mismatches 128; Indels 13; Gaps 5;

QY 63 LVH-----GKNPDVROLTLTEIFMKDPEQEFMQAVREVAVSLQPVFEKRPPELLP--IP 114
Db 11 LIHYAEDRALKYNLNEFLNYVQARDPHQDEFLQAVEEVMTSLWPFIEKQPEVAEQGLL 70
QY 115 KQIVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAF 174
Db 71 ERLVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAF 130
QY 175 EQIFKNSLTTLPMGGGKGSDPDPKGSDAEVRMPCOSFMTLORHISYVQDVDPAGDIGV 234
Db 131 EQTFKNSLTTLPMGGGKGSDPDPKGSDAEVRMPCOSFMTLORHISYVQDVDPAGDIGV 190
QY 235 GAREIGVLFQYKRITKNYTGVLTPKGOEYGGSEIRPEATGYGAVLFVENVLDKGESLKG 294
Db 191 GAREVYGMAGMMKKLSNDTACVFTGKISFGSLMRPEATGYGVYFABEMLKTRGQSF 250
QY 295 GKRCVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNS 354
Db 251 KGTVSISSGSGNVAQYAAEKAMFLGAKVVTLSDSNGTVYVKNKGTDELLAEVMEKNIKR- 309
QY 355 ARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEHDAELLLKHGCGVYVVGAN 414
Db 310 GRISFASKHGFYFEGKTPMHI--PVDIALPCATQNEIDTGEDAKTLIANGVICVAEGAN 367
QY 415 MPSTNEAIHKYNKAGIICPGKAAAGGAVSGLMNTQNRMSLNWTRREVRDKLERIMK 474
Db 368 MPSTLEAVEHFIEAKILYAPKASNAGGAVTSGLEMSQNAIRLGTWTRAEVDERLHAIMKD 427
QY 475 IYDSAM--GPSRRYVVDLAAGANIAGFTKVADAVKAQGV 510
Db 428 IHANCVRYGTGEDGTVNVVDGANIAGFVKVADAVKAQGV 465
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/ FILING DATE: 01-JUL-1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/021,058
/ FILING DATE: 02-JUL-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kokulis, Paul K.
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: 81163/241766
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)-861-3503
/ TELEFAX: (202)-822-0944
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 447 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
US-08-886-640-3

Query Match 45.5%; Score 1201; DB 2; Length 447;
Best Local Similarity 54.0%; Pred. No. 2.9e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;
QY 72 VQLLTETPMKDPQOEQFMAQVREAVASLPQVFEKPEL--LPFKQIVPEPVTFRVS 129
DB 7 LESFLNHVQRDPNQTPEFAQVREVTTLWPFLEQNPKYRQMSLLERLVEPERSVIOFRV 66
QY 130 WLDADGNLQVNRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIPKNSLTTLPMGG 189
DB 67 WYDDNRQIQVNRAMRVQFSSAIGPYKGNRFHPSVNLISILKFLGFEQTFKNAITLPMGG 126
QY 190 KGKGSDFDPKGSDAEVRMFCQSPMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 249
DB 127 KGKGSDFDPKGSSEGVNRFQALMTLYRHLGADTDVPAGDIGVGREGVGMAGMMKKL 186
QY 250 TKNYTGVLTPKGOEVGSGEIRPEATGYCAVLFEVNLKDKGSLKGRCLVSGAGNVAQY 309
DB 187 SNNTACVFTGKLSFGSLIRPEATGYGLVYFTTEAMLRKHGMFGFEGMRVSVSGSNVAQY 246
QY 310 CAELLEKGAIVLSLSDSGYVVEPNFTREQLQAVQDMKKNNNSARISEYKSDTAVVVG 369
DB 247 ALEKAMEFGARVITASDSGTVVDESFTKEKLARLIEI-KASRGRVADYAKEGLVYL 305
QY 370 DRKRWELDCQVDIAPPQATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 429
DB 306 EQQPWSL--PVDIALPCATQNELDVDAHQIANGVKAABEGANMPTTIEATELFPQAG 363
QY 430 ILYCPGKAANAGGAVSGLEMTQNRMSLNWTRVEVRDKLERIMKDIYDSAM---GPSRRY 486
DB 364 VLFAPGKAANAGGAVATSGLEMAQNAARLGWKAEBKVDARLHHIMLDIHACVDHGGEGBQT 423
QY 487 NYDLAAGANIAGFTKVADAVKAQAGV 512
DB 424 N--YVQGANIAGFVKVADAMLAQGV 447

RESULT 14
US-08-884-235-11
/ Sequence 11, Application US/08884235
/ Patent No. 6329573
/ GENERAL INFORMATION:
/ APPLICANT: Lightfoot, David A.
/ APPLICANT: Long, Lynn M.
/ APPLICANT: Lightfoot, Maria E. Vidal
/ TITLE OF INVENTION: PLANTS CONTAINING THE gdhA GENE AND
/ TITLE OF INVENTION: METHODS OF USE THEREOF
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pillsbury Madison & Sutro, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington

/ STATE: D.C.
/ COUNTRY: United States of America
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MS Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/884,235
/ FILING DATE: 27-JUN-1997
/ CLASSIFICATION: 800
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 447 residues
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
US-08-884-235-11

Query Match 45.5%; Score 1201; DB 3; Length 447;
Best Local Similarity 54.0%; Pred. No. 2.9e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;
QY 72 VQLLTETPMKDPQOEQFMAQVREAVASLPQVFEKPEL--LPFKQIVPEPVTFRVS 129
DB 7 LESFLNHVQRDPNQTPEFAQVREVTTLWPFLEQNPKYRQMSLLERLVEPERSVIOFRV 66
QY 130 WLDADGNLQVNRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIPKNSLTTLPMGG 189
DB 67 WYDDNRQIQVNRAMRVQFSSAIGPYKGNRFHPSVNLISILKFLGFEQTFKNAITLPMGG 126
QY 190 KGKGSDFDPKGSDAEVRMFCQSPMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 249
DB 127 KGKGSDFDPKGSSEGVNRFQALMTLYRHLGADTDVPAGDIGVGREGVGMAGMMKKL 186
QY 250 TKNYTGVLTPKGOEVGSGEIRPEATGYCAVLFEVNLKDKGSLKGRCLVSGAGNVAQY 309
DB 187 SNNTACVFTGKLSFGSLIRPEATGYGLVYFTTEAMLRKHGMFGFEGMRVSVSGSNVAQY 246
QY 310 CAELLEKGAIVLSLSDSGYVVEPNFTREQLQAVQDMKKNNNSARISEYKSDTAVVVG 369
DB 247 ALEKAMEFGARVITASDSGTVVDESFTKEKLARLIEI-KASRGRVADYAKEGLVYL 305
QY 370 DRKRWELDCQVDIAPPQATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 429
DB 306 EQQPWSL--PVDIALPCATQNELDVDAHQIANGVKAABEGANMPTTIEATELFPQAG 363
QY 430 ILYCPGKAANAGGAVSGLEMTQNRMSLNWTRVEVRDKLERIMKDIYDSAM---GPSRRY 486
DB 364 VLFAPGKAANAGGAVATSGLEMAQNAARLGWKAEBKVDARLHHIMLDIHACVDHGGEGBQT 423
QY 487 NYDLAAGANIAGFTKVADAVKAQAGV 512
DB 424 N--YVQGANIAGFVKVADAMLAQGV 447

RESULT 15
US-08-370-193A-11
/ Sequence 11, Application US/08370193A
/ Patent No. 5573945
/ GENERAL INFORMATION:
/ APPLICANT: ONO, EIJI
/ APPLICANT: TSUJIMOTO, NOBUHARU
/ APPLICANT: MATSUI, KAZUHIKO
/ APPLICANT: KURAHASHI, KAZUHIKO
/ TITLE OF INVENTION: MUTANT AND METHOD FOR PRODUCING
/ TITLE OF INVENTION: L-GLUTAMIC ACID BY FERMENTATION
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
/ ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,193A
FILING DATE: 09-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-714-0
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-370-193A-11

Query Match 45.5%; Score 1200; DB 1; Length 447;
Best Local Similarity 54.0%; Pred. No. 3.6e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;
QY 72 VRLQLTEIFMKDPEQOEFMQAVREAVSLQPVFEKEPEL--LPPIFKQIVPERVITFRYS 129
Db 7 LESFLNHVQKDPNQNPQTEFAQAVREVTTLWPFLEQNPKYRQMSLLRELVEPERVIQFRVY 66
QY 130 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPVNLISIMKFLAFQIFKNSILITLPMGG 189
Db 67 WDDRNQIQVNRARVQPSAIGPYKGNRFPSPVNLISILKFLGFEQTFKALITLPMGG 126
QY 190 GKGGSDFDPKGSDDAEVMPFCQSMTELQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 249
Db 127 GKGGSDFDPKGSSEGVMEFQALMTELYRHLGADTDVPAGDIGVGREVGFMGMKKL 186
QY 250 TKNYTGVLTPKGOEYGGSEIRPEATGYGAVLPVENVLKDGESLKGKRCCLVSGAGNVAQY 309
Db 187 SNTACVFTGKGLSFGGSLIRPEATGYGLVYFTEAMLKRHGMFGEMRVSVSGGNVAQY 246
QY 310 CAELLLEKGAIVLSLSDSQGYVVEPNQFTREOLQAVODMKKNNSARISEYKSDTAVVYG 369
Db 247 AIEKAMEFGARVITASDSSGTVDDESQFTKEKLRLIEI-KASRGRVADYAKEFGLVYL 305
QY 370 DRKPELDCQVDIAFPCCATQNEIDSHDAELIKHGQYVVEGANMPSTNEAIHKYNKAG 429
Db 306 EQQPWSL--PVDIALPCATQNELDVAHQHANGVAVKAVESGANMPTTIEATLFFQQAG 363
QY 430 IYICPGKAANAGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAM---GPSRRY 486
Db 364 VLFAPGKAANAGGVATSGLEMPQNAARLGLWKAQKVDARLHIMLDIHHACVHGGEQGT 423
QY 487 NVDLAAGANIAGFTKVADAVKAQAV 512
Db 424 N--YVQGANIAGFVKVADAMLAQGV 447

Search completed: September 8, 2005, 02:12:06
Job time : 30.4224 secs

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Query Match 48.8%; Score 1286.5; DB 2; Length 470;
Best Local Similarity 55.2%; Pred. No. 8e-79; Indels 19; Gaps 7;
Matches 266; Conservative 64; Mismatches 133;

Qy 34 ISAMDATTDFTALQKAVKQMAKTAGTEGLVHGINKPNDVROLITLIFMKDPEQOEPMQAV 93
Db 1 MSALMDKTRFRVVLQK-----NASVYESLV-----DQENNNYERMKLDPNQVETLQAF 50

Qy 94 REVANSLOQVFEKREKPELLPIFKQIYPERVITFRVSWLDDAGNLQVNRGRVOYSSAIDP 153
Db 51 HETLSLKDELFMEEPKYLPILITLSEPERAIOFRVCLMDNGVQRKRCFRVQYNSALGP 110

Qy 154 YKGLRHFHSVNLSTIMKFLAFROIENKSLTTLPMGGCKGSDPDPKGSADAEYMRQCSF 213
Db 111 YKGLRHFHSVNLSTIVKFLAFROIENKSLTTLPMGGCKGSDPDPKGSADAEYMRQCSF 170

Qy 214 MTELQNHISYVDVPAAGDIGVAREIGVLFQGYKRTTKNYTGVLPKGOEYGSSEIRPA 273
Db 171 KMELVNHIIGPCTDVPAGDIGVAREIGVLYGYKKI VNSPNTLTGKNVKGSSNLRVYA 230

Qy 274 TGYGAVLFEVNTLKDKGESLKGKCLVSGAGVAVQYCAELLLEKALIVLSDSQGYVE 333
Db 231 TGYGAVLFEVNTLKDKGESLKGKCLVSGAGVAVQYCAELLLEKALIVLSDSQGYVE 290

Qy 334 PNGFTREOLQAVQDMKKKNSARISRY--KSDTAVVGDPRKRPWELDQVDIAFPATON 391
Db 291 PNGFTRENLPLDLKEB--KKGRIKSYLNHSSYAKYF--DNEKRWGVPCC--TLAFCATON 346

Qy 392 EIDEHDAELLIKHGCQYVEGAMNPSTNEAIHKYKAGIYCPGKANAAGVAVSGLEMT 451
Db 347 EINDLEBAKLQKNGCGLVGEANMPSTVDALNIFKNNITTYCRSKAANGVAVLSGLEMS 406

Qy 452 QNRMSLNTREBYRDKLERIMKDIYDAMGPSRRY--NVDLAAGANIAGFTKVADAVKA 508
Db 407 QNFQESHMTREYDEKLKEIMENIFACSENLKTYKNKYDLOAGANIGFLKVAESYIE 466

Qy 509 OG 510
Db 467 OG 468

RESULT 13
Q923C4 PRELIMINARY; PRT; 445 AA.
AC Q923C4;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE NADP-glutamate dehydrogenase (BC 1.4.1.4).
GN Name-gdhA;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAC1;
RA Ansari F.;
RL Thesis (1994), University of London London U.K.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PAC1, and PAOI;
RA Brown P.R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=PAOI;
RA Ansari F.;
RL Thesis (1994), University of London, London U.K.
DR EMBL; Y18494; CAA7192.1; -
DR EMBL; Y15166; CAA75437.1; -
DR HSSP; P24295; IADP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog; 1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFVHDRCANSE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
DR Oxioreductase.
SQ SEQUENCE 445 AA; 48532 MW; B00DDBE8D3A06D8A CRC64;

Query Match 48.7%; Score 1285; DB 2; Length 445;
Best Local Similarity 58.4%; Pred. No. 9.4e-79;
Matches 261; Conservative 56; Mismatches 118; Indels 12; Gaps 5;

Qy 72 VROLTTELFMKDPEQOEPMQAVREAVAVLQVFEKREPLLPI--IPKQIYPERVITFRVS 129
Db 5 VDAFLERLKRDPDPPRPHQAVEBVLRLMFLFLEANPHYLEAGITLIVERPERALIFRVP 64

Qy 130 WDDAGNLQVNRGRFRVOYSSAIGPYKGLRPHPSVNLSTIMKFLAFROIENKSLTTLPMGG 189
Db 65 WDDQGRVVRVNRGYVQSSAIGPYKGLRPHPSVNLGVTLKFLAFROIENKSLTTLPMGG 124

Qy 190 GKGSDFDPKKSDEUNRFGQSPFTELQNHISYVDVPAAGDIGVAREIGVLFQGYKRI 249
Db 125 GKGSDFDPKKSDEUNRFGQSPFTELQNHISYVDVPAAGDIGVAREIGVLFQGYKRI 184

Qy 250 TKNYGVTLTPKGOEYGSSEIRPEATYGAFLFEVNTLKDKGESLKGKCLVSGAGVAVQY 309
Db 185 SNQFISVLTGKGLSGLSLIRPEATYGAFLFEVNTLKDKGESLKGKCLVSGAGVAVQY 244

Qy 310 CAELLLEKALIVLSDSQGYVEPNFTREOLQAVQDMKKKNSARISRYKSDT--AV 366
Db 245 AARKVMENMGKVISLSDSEGLTYAAGLSDEQWEYIMELK---NARAGHPDVGVEQPSL 300

Qy 367 YVGDPRKRPWELDQVDIAFPATONEIDEHDAELLIKHGCQYVEGAMNPSTNEAIHKYN 426
Db 301 QFLBGPVPMGLAC--DILPCTQNELDAEDRRLLNAGCVAVGAMNPSTLEVDLPL 358

Qy 427 KAGIYCPGKANAAGVAVSGLEMTQNRMSLNTREBYRDKLERIMKDIYDAMGPSRR 485
Db 359 EAGIITYABGKASMGAGVAVSGLEMSQNMRLRMSGSEVDTKLHGIMQSIHACILYGBEQ 418

Qy 486 YNVDLAAGANIAGFTKVADAVKAQGA 512
Db 419 GRVNVYKGANIAGFYKVADAMLAQGV 445

RESULT 14
Q7YZU7 PRELIMINARY; PRT; 437 AA.
AC Q7YZU7;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Glutamate dehydrogenase (Fragment).
GN Name-gdh;
OS Trichomonas vaginalis.
OC Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;
OC Trichomonadidae; Trichomonadinae; Trichomonas.
OX NCBI_TaxID=5722;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=12820901; DOI=10.1186/1471-2148-3-14;
RA Andersson J.O.; Roger A.J.;
RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes";
RL BMC Evol. Biol. 3:14-14(2003).
DR EMBL; AF533886; AAP83853.1; -
DR HSSP; P24295; IADP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.

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QY 190 GKGSDFDPKSKDAEYMRFCQSEFMTLQHHISYVODVPAGDIGVAREIGYFGQYKRI 249
DB 128 GKGSDFDPKSKDAEYMRFCQAFMSSELYRHIGADCCVPPAGDIGVAREIGFPMFGYKRL 187
QY 250 TKNYTGLTPKGGEGYGGSEIRPEATGGAULTFVENYLDKDGESLKGRCCLVSGAGNVAOY 309
DB 188 ANQFTSVLTCKGMYTGGSLRPRATYGCYCFABEMLKRDKRI DGRVAVSGSGNVAOY 247
QY 310 CAELILEKGAIVLSLSDSQGYVEPNQFTREQLQAVODMKKNNNSARISEKSDTAVYVG 369
DB 248 AAKRWMDLGGKIVLSLSSECTIYAEAGLTQAQMDALMELKNVGR-GRISLDAQFGLEFR 306
QY 370 DRKPEWELDCQVDIAFPATONEIDEHDAELIKHGQCYVVGANMPSTNEAIHKYNKAG 429
DB 307 KQGTFWMLPC--DIALFCATONEIGADARTLLRNGCI CVAEGANMPTTLEAVDIFLDAG 364
QY 430 IITCPGAANAAGVAAVSGLEMTQNRMSLMTREBYDKLERIKMDIYDSAM--GPSRRYN 487
DB 365 ILVAPGASNAAGVAAVSGLEMSQANMLMTAGBVSCKLNNIQTSHHACVHYGBEADGR 424
QY 488 VDLAAGANIAGFTKVADAVAKAGAV 512
DB 425 INVYKGANIAGFTKVADAMLAQGVV 449

RESULT 11
O96940 PRELIMINARY; PRT; 470 AA.
ID O96940;
AC O96940;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DB 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DB Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
Name=GLUDH; Synonyms=GDH;
Plasmodium falciparum.
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxId=5833;
RX MEDLINE=99089647; PubMed=9874251;
RA Wagner J.T., Niedemann H., Faerber P.M., Lotspeich F.,
RA Krauch-Siegel R.L.;
RT "Glutamate dehydrogenase, the marker protein of Plasmodium falciparum.
RT Cloning, expression and characterization of the malarial enzyme.";
RL Bur. J. Biochem. 258:813-819(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Li L.H., Li M., Wu Y.S., Wang P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL; Y12927; CAA73390.1; -.
DB EMBL; AY040586; AAK77969.1; -.
DR HSSP; P24295; IADP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog_C.
DR InterPro; IPR006096; GLFV_dehydrog_N.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N_1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

Query Match 48.8%; Score 1286.5; DB 2; Length 470;
Best Local Similarity 55.2%; Pred. No. 8e-79;
Matches 266; Conservative 64; Mismatches 133; Indels 19; Gaps 7;

QY 34 ISAMDITTDGFTLQAVKQMAKATGEGYHGIKNPVDVRLQTLTFMDPBEQDEQNAV 93
DB 1 MSALKDKTGRFVVLDR-----NASYVESIV----DOENNVYERVMKLDPNQVEFTLQAF 50

```

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QY 94 REVAVSLQVFEKRPPELLPIFKQIVEPERVITFRVSWLMDAGNLQVNRGFRVQSSAIGP 153
DB 51 HEILVSLKTLFMEEPKYLPIIETLSRPERALQPRVCMLDNGVQRNRCFRVQYNALIGP 110
QY 154 YKGGILFPHSPVNLSTINKFLAFBOIFKNSLTTLPMGGCKGSDPDPKSKDAEYMRFCQSF 213
DB 111 YKGGILFPHSPVNLSTINKFLAFBOIFKNSLTTLPMGGCKGSDPDPKSKDAEYMRFCQSF 170
QY 214 MRELQHHISYVODVPAGDIGVAREIGYFGQYKRI TKNYTGLTPKGGEGYGGSEIRPEA 273
DB 171 MRELQHHISYVODVPAGDIGVAREIGYFGQYKRI TKNYTGLTPKGGEGYGGSEIRPEA 230
QY 274 TGYGAVLTFVENYLDKDGESLKGRCCLVSGAGNVAOYCAELILEKGAIVLSLSDSQGYVE 333
DB 231 TGYGAVLTFVENYLDKDGESLKGRCCLVSGAGNVAOYCAELILEKGAIVLSLSDSQGYVE 290
QY 334 PNGFTREQLQAVODMKKNNNSARISEY--KSDTAVYVGDGRKPEWELDCQVDIAFPATON 391
DB 291 PNGFTREQLQAVODMKKNNNSARISEY--KSDTAVYVGDGRKPEWELDCQVDIAFPATON 346
QY 392 EIDEHDAELIKHGQCYVVGANMPSTNEAIHKYNKAGIITYGRKANAGVAVSGLEMT 451
DB 347 EIDEHDAELIKHGQCYVVGANMPSTNEAIHKYNKAGIITYGRKANAGVAVSGLEMT 406
QY 452 QNRMSLMTREBYDKLERIKMDIYDSAMGPSRRY---NVDLAAGANIAGFTKVADAVKA 508
DB 407 QNFPQSHMTREBYDKLERIKMDIYDSAMGPSRRY---NVDLAAGANIAGFTKVADAVKA 466
QY 509 QG 510
DB 467 QG 468

RESULT 12
Q81LT0 PRELIMINARY; PRT; 470 AA.
ID Q81LT0;
AC Q81LT0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB NADP-specific glutamate dehydrogenase.
GN ORFNames=PP14_0164;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxId=36329;
RX MEDLINE=2255705; PubMed=1236864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung B., White O., Bertram M., Hyman R.W.,
RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Risen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,
RA Chan M.S., Nene V., Shallow S.O., Suh B., Peterson J., Angiolli S.,
RA Perlea M., Allen J., Selengut J., Harte D., Mather M.W., Valdivia A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DB EMBL; AE014818; AAN36776.1; -.
DR HSSP; P24295; IADP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog_C.
DR InterPro; IPR006096; GLFV_dehydrog_N.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N_1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

```


Db	302	YEFKQKPGV--AAETALPCATONEIDDEAATLTLANGLVVAEGNMPSTTGA	YQF	428	AGIYCPKKAANAGVAVSGLEMTONRMSLNTMREVRDKLERIMEDYDSAMGSPRRY	486
Db	360	AGTLVAPGKASVAGVAVTSGLEMSQNALILSTTREVDRLGIMGSHESCL---	KYG	487	---NVDLAAGANIAGFTKVDAYAAQ	510
Db	416	KVGDVTNYYVNGANIAGFVKVADAMLAAQ	443			
RESULT 9						
	90JUT56	PRELIMINARY;	PRT;	444	AA.	
AC	90JUT56;					
DT	01-OCT-2000 (TREMBLrel. 15, Created)					
DT	01-OCT-2000 (TREMBLrel. 25, Last sequence update)					
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)					
DE	Glutamate dehydrogenase (EC 1.4.1.4).					
GN	Name=gda; OrderedLocusNames=NNAL1964;					
OS	Neisseria meningitidis (serogroup A).					
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;					
OK	Neisseriaceae; Neisseria.					
OK	NCBI_TaxId=65699;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Z2491 / Serogroup A / Serotype 4A;					
RX	MEDLINE=20222556; PubMed=10761919, DOI=10.1038/35006655;					
RA	Parthill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,					
RA	Klee S.R., Metcalf G., Basham D., Brown D., Chillingworth T.,					
RA	Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holtroyd S.,					
RA	Jagels K., Leather S., Moulé S., Mungall K.L., Quail M.A.,					
RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skellon J.,					
RA	Whitehead S., Spratt B.G., Barrall B.G.;					
RT	"Complete DNA sequence of a serogroup A strain of Neisseria					
RT	meningitidis Z2491".					
RL	Nature 404:502-506(2000).					
DR	EMBL, AL162757; CAB85184.1; -.					
DR	PIR: B81825; B81825.					
DR	HSSP: P24295; IAMP.					
DR	GO: 00004354; F:glutamate dehydrogenase (NADP+) activity; IEA.					
DR	GO: 0016491; F:oxygen oxidoreductase activity; IEA.					
DR	GO: 0006520; P:amino acid metabolism; IEA.					
DR	InterPro: IPR006095; GLFV_dehydrog.					
DR	InterPro: IPR006096; GLFV_dehydrog.					
DR	InterPro: IPR006097; GLFV_dehydrog.					
DR	InterPro: IPR006097; GLFV_dehydrog.					
DR	Pfam: PF00208; GLFV_dehydrog.					
DR	Pfam: PF02812; GLFV_dehydrog.					
DR	PRINTS: PR00082; GLFDHDSGNASE.					
DR	PROSITE: PS00074; GLFV_DEHYDROGENASE; 1.					
KW	Complete proteome; Oxidoreductase					
SEQUENCE	444 AA; 48462 MM; DE7FLA7B8DD6f424 CRC64;					
Query Match						
	49.1%;	Score 1294.5;	DB 2;	Length 444;		
	Best Local Similarity	57.1%;	Pred. No. 2.1e-79;			
	Matches 256;	Conservative 72;	Mismatches 105;	Indels 15;	Gaps 6	
QY	71	DYRQLLTIFMKDPEQOEFMQAVREYAVSLQVFEKRPBL--PIKQIYEPERVITFRY	128			
Db	3	DNLTLFANLKQNNPNDEPHQAVEEVEFMSLDFLANPKYTOOSLIERIYEPERVVMFRV	62			
QY	129	SWLDAGNLQVNRGPFVVOYSSAIGPVKGGIRFPSPVNLISMKFLAPEQIFKNSLTLLPMG	188			
Db	63	TVQDDKGVQVNRGRVQWSSAIGPYKGGIRFPFTVDLGLVFLAEQVFKNALITLLPMG	122			
QY	189	GKGGSDFDPKKSADAEVNRFCOSFWTELQRIHSYQVDPVAGDIGVAREIGYLFQGYR	248			
Db	123	GKGGSDFDPKKSADAEVNRFCQAFMTLYRHHGADTVDPAGDIGVGRRTIGYLFQGYR	182			
QY	249	ITKNTTGVITPVGQEYGGSEIRPEATGYGAVLFEVAVLKDKGSLGKRCVLVSGAGNVAQ	308			
Db	183	INNEPSVLTGGLGEMGSLIRPEALGYGVVFAQMLQYRNDSPGKRTVLISGSGNVAQ	242			

Oy		369	CCAGLLEKKAIVLSTLSGQGVYPER-NGPTREOUQAOMDKKKNNRARSISYSKDITAY	367
Dd		243	YAAEAGIOLGAKVLLVSNSNGVLFPDSGMSEAQLAAILTELKVRRE-RVATYAEQGLO	301
Oy		368	VGDRRKPPELIDCOVDIAFPCATONEIDHDDELLIKHGCGOYVEGANNPSTEALHKYNK	427
Dd		302	YFENQKPGV--AAEIALPCTONELDBEAKTILLANGCYVAEGANNPSTIGAVEQFIK	359
Oy		428	AGIIYCPEKANAGAVAVSGLPMTONRMSLWMTREEVPDKLERIMKDIYDSAMGPSRY-	486
Dd		360	AGIIYAPKASNAGGAVTSGLEMSGONAIRLSTWREEVDQRLFGIMQSIHESCL-----KYG	415
Oy		487	----NVDLAAGANTAGFTKVADAVYAOG	510
Dd		416	KVGDTVNYYNAGNIAGPVKADVADAMLDAQ	443
 RESULT 10 088023				
ID	088023	PRELIMINARY;	PRT;	449 AA.
AC	088023;			
DT	01-JUN-2003	(TREMBLrel. 24, Created)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE		Glutamate dehydrogenase,		
CN	Name=gdh,	OrderedLocusNames=PP0675;		
OS	Pseudomonas putida	(strain KT2440).		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
OC	Pseudomonadaceae; Pseudomonas.			
OX	NCB1_Taxid=160488;			
RN	[1]			
RP		SEQUENCE FROM N.A.		
RX	MEDLINE=22423060;	PubMed=12534463;		
RA	Nelson K.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,			
RA	Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,			
RA	Brinkac L.M., Benson M.C., Debey R.T., Daugherty S.C., Kolonay J.F.,			
RA	Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,			
RA	Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,			
RA	Moazzer A., Utechtack T.R., Rizzo W., Lee K., Kosak D., Moestl D.,			
RA	Weidler H., Labber J., Stjepandic D., Hohneisel J., Streletz M., Helm S.,			
RA	Kiewit C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,			
RA	Frazer C.M.;			
RT	"Complete genome sequence and comparative analysis of the			
RT	metabolically versatile Pseudomonas putida KT2440."			
RL	Environ. Microbiol. 4:799-808(2002).			
DR	EMBL; AE016776; AAN6300.1; -			
DR	HSSP; P24295; IAUJ.			
DR	TIGR; PP0675; -			
DR	GO; GO:0016491; P:oxidoreductase activity; IEA.			
DR	GO; GO:0006520; P:amino acid metabolism; IEA.			
DR	InterPro; IPRO06095; GLFV_dehydrog.			
DR	InterPro; IPRO06096; GLFV_dehydrog_C.			
DR	InterPro; IPRO06097; GLFV_dehydrog_N.			
DR	Pfam; PF00208; GLFV_dehydrog_1.			
DR	Pfam; PF02812; GLFV_dehydrog_N_1.			
DR	PRINTS; PR00082; GLEPHDGNASE.			
DR	PROSITE; PS00074; GLFV_DEHYDROGENASE, 1.			
KW	Complete proteome.			
SQ	SEQUENCE 449 AA; 48871 MW; EF1733B6ABC89627 CRC64;			
 Query Match 48.8%; Score 1287.5; DB 2; Length 449; Best Local Similarity 58.2%; Pred No. 64e-79; Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4				
Oy		72	VROLTLTEFMDOPEOEPMQAVREYVASLPVFEXRPELLP--IFKQIVEPERVITERVS	129
Dd		8	VDNFLARKORBDQCPERFHQAAVEEVILRTLPLLEANPHYLQSIGIERMWEPRRAVLFVRS	67
Oy		130	WLDDAGNIGNVNRGRFVYSSAIGPKKGIGLRFRPSNYLSIMKEIARPEQIRKNSLTLLPMWG	189
Dd		68	WDDDGKQVQVNRGYRIQWSSSAIGPKGGIGLRFRPSNYLSVLKFLAFEPQVKNSLTSLPMWG	127

ID	Q88023	PRELIMINARY;	PRT;	449 AA.
AC	Q88023;			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Glutamate dehydrogenase.			
OS	Name=gdhA, OrderedLocustNames=PP0675;			
OC	Pseudomonas putida (strain KT2440).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
OC	Pseudomonadaceae; Pseudomonas.			
OX	NCBI_TaxID=160488;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22423060; PubMed=12534463;			
RA	Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hildbert H.,			
RA	Marins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,			
RA	Birkack L.M., Beaman M.J., Debay R.T., Daugherty S.C., Kolonay J.F.,			
RA	Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,			
RA	Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,			
RA	Moazzer A., Utechtack T.R., Rizzo M., Lee K., Kosack D., Moestl D.,			
RA	Wedler H., Lamber J., Stjepandic K., Huetzel J., Streitz M., Helm S.,			
RA	Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmiller B.,			
RA	Fraser C.M.;			
RT	"Complete genome sequence and comparative analysis of the			
RL	metabolically versatile Pseudomonas putida KT2440.";			
RL	Environ. Microbiol. 4:799-808(2002).			
DR	EMBL; AE016776; AAN6300.1; -			
DR	HSSP; P24295; IAU.			
DR	TIGR; PP0675; -			
DR	GO; GO:0016491; P:oxidoreductase activity; IEA.			
DR	GO; GO:0006520; P:amino acid metabolism; IEA.			
DR	InterPro; IPR006095; GLFV_dehydrog.			
DR	InterPro; IPR006096; GLFV_dehydrog_C.			
DR	InterPro; IPR006097; GLFV_dehydrog_N.			
DR	Pfam; PF00208; GLFV_dehydrog_1.			
DR	Pfam; PF02812; GLFV_dehydrog_N_1.			
DR	PRINTS; PR00082; GLFDHDKNASE.			
DR	PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.			
DR	Complete proteome.			
SQ	SEQUENCE 449 AA; 48871 MW; EF1733BAEC89627 CRC64;			
QY	Query Match	48.8%;	Score 1287.5;	DB 2; Length 449;
QY	Best Local Similarity	58.2%;	Pred. No. 6.4e-79;	
QY	Matches 259; Conservative 55; Mismatches 124;		Indels 7;	Gaps 4
QY	72 VRQLLTLEFMDDPEQEFMQAVREYAVSLDPYFEKRPBLLP--IFKQIVPERVITFRVS 129			
QY	8 VDNFIALRKQNDPQGPPEFHQAEEVYLRITLMPLEANPHYLQSGILREMYEPRRAVLFVRS 67			
QY	130 WDDDGNGNTQVNRGPFVQYSSAIGPRKGGIRFRFPNVLSTMKELAPQIRKNSLTLLPMWG 189			
QY	68 WDDDGKQVQVNRGYPRIQSSSAIGPKGGIRFRFPNVLSTMKELAPQIRKNSLTLLPMWG 127			

ID	Q9HUJ7	PRELIMINARY;	PRT;	445 AA.
AC	Q9HUJ7;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
D8	Glutamate dehydrogenase.			
GN	Name=gdhA; OrderedLocusNames=PA4568;			
O8	Pseudomonas aeruginosa.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
OX	Pseudomonadaceae; Pseudomonas.			
RX	NCB1_Taxid=287;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 15692 / PAOI;			
EX	MEDLINE=20437337; PubMed=10984043; DOI=10.1038/350233079;			
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Muzoguchi S.D., Warrenner P.,			
RA	Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,			
RA	Gardner R.L., Collier L., Tolentino E., Westbrook-Wedman S., Yuan Y.,			
RA	Brody L.L., Coulter S.N., Polger K.R., Kas A., Latig K., Lim R.M.,			
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,			
RA	Reizer J., Salier M.H., Hancock R.E.W., Iori S., Olson M.V.;			
RT	"Complete genome sequence of Pseudomonas aeruginosa PAOI, an			
RL	opportunistic pathogen.";			
RL	Nature 406:958-964(2000).			
DR	EMBL; AE004872; AAC07976.1; --			
DR	PIR; H83072; H83072.			
DR	HSSP; P24295; IAUP.			
DR	GO; GO:0016491; F:oxygenoreductase activity; IEA.			
DR	GO; GO:0006520; P:amino acid metabolism; IEA.			
DR	InterPro; IPRO06095; GLFV_dehydrog.			
DR	InterPro; IPRO06096; GLFV_dehydrog_C.			
DR	InterPro; IPRO06097; GLFV_dehydrog_N.			
DR	pfam; PF00208; GLFV_dehydrog_1.			
DR	pfam; PF02812; GLFV_dehydrog_N_1.			
DR	PRINTS; PR00082; GLFDHGNASE.			
DR	PROSITE; PS00074; GLFV_DEHYDROGNASE; 1.			
KY	Complete proteome.			
SQ	SEQUENCE 445 AA; 48856 MW; 643EB12BC84F3418 CRC64;			
Query Match	49.6%; Score 1309; DB 2; Length 445;			
Best Local Similarity	59.2%; Pred. No. 2,2e-80;			
Matches 263; Conserved	55; Mismatches 120; Indels 6; Gaps 4;			
Qy	72 VRQLLTIFMKDPBQOEAFMOAVREVAVALOPFEKRPPLLP--IPKOIVBERVITPFVS 129			
Dd	5 VDAFLERLKRRDDPDPEFHQAIVEVLRSLLMPLLEPNPHYLEGILIERIIVERBALFFVP 64			
Qy	130 WLDDAGNLQNVRGFVVYSSAIGPYKGLRHPSVNLSIMKFLAEQIFKNSLTTLPMGG 189			
Dd	65 WVDDGRRVRNVRGVQMSSAIGPKGGLRHPSNVLTGLFLAEQVFKNSLTTLPMGG 124			
Qy	190 GKGSDFPPFKKSDEEVMRFCSFWTELORHSIVYQVDPADDIGVAEEIGYLFGQYRI 249			
Dd	125 GKGSDFPPFKKSDEEVNRFCQSFENSELYRVHGADLDVPADDIGAAEIGYLFGQYRL 184			
Qy	250 TKNYTGVLTPKQOEGSGSEIRPEATGYAVLVFENVLKDKESSLKGRCLTVSGAGNAVQY 309			
Dd	185 SNQFTSVLTGKGLSGSLIRPEALGFPCVYFAQOMLMDRGRPGCGQVALISGSGNAVQY 244			
Qy	310 CAELLERGAIVLSDSQGYVEBPNGFTTBOLQAVQDMKKNNASRISEYKSDTAAYVG 369			
Dd	245 AARKWMEGWGKYVISISDSBETGLYAAGLSDQEWEYMLKYNVR-GRIREMAEQESLQFL 303			
Qy	370 DRKKPWLDCQVDIAFPCATONEIDEHAAILIKGCQYVVEGANMPSTNAIRKNAAG 429			
Dd	304 EGRRPFWGLAC--DIALPCATONEIDAEARRILLANGCVVAEGANMPSTLAIVDLFLAEG 361			
Qy	430 IIYCPGKAANKGVAVSGLEMTQRMSLNMTREEVRDLTSRKMDIYOSA-MGPSRRRYNV 488			
Dd	362 ILIYAPGRKSNAGVAVSGLEMSQNNAMLRMSBEGEVDVTYLGHTIMOSIHACLLYGBEQQRV 421			
Qy	489 DLAAGANIAGFTKVADAIVAKQAAV 512			

Db 422 NYVKANNTAGFVKVADMLAQGV 445

RESULT 8

09JY71 PRELIMINARY; PRT; 444 AA.

ID 09JY71

AC 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Glutamate dehydrogenase, NADP-specific.

GN Ordered locus names=NM1710;

OS *Neisseria meningitidis* (serogroup B).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; *Neisseria*.

OX NCBI_TaxID=491;

RM [1]

RP SEQUENCE FROM N. A.

RC STRAIN=MC58 / Serogroup B;

RK MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;

RA Tetteiln H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,

RA Nelson K.E., Sisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,

RA Dodson R.J., Nelson W.C., Gwin M.L., Debay R.T., Peterson J.D.,

RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,

RA Dougherty B.A., Mason T.M., Clecko A., Parksey D.S., Blatt E.,

RA Clifton H., Clark E.B., Cotton M.D., Uettermack T.R., Khouri H.M.,

RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rapnold R.,

RA Venter J.C.;

RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain

RT MC58.";

RL Science, 287:1809-1815(2000).

DR EMBL; AE002521; AAF42057.1; -.

DR PIR; H81050; H81050.

DR HSSP; P24295; LAUP.

DR TIGR; NM1710; -.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006520; P:amino acid metabolism; IEA.

DR InterPro; IPR006095; GLFV_dehydrog.

DR InterPro; IPR006096; GLFV_dehydrog_C.

DR InterPro; IPR006097; GLFV_dehydrog_N.

DR Pfam; PF00208; GLFV_dehydrog_1.

DR Pfam; PF02812; GLFV_dehydrog_N_1.

DR PRINTS; PR00082; GLFV_HDRGNASE.

DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.

DR KW Complete proteome.

SEQ SEQUENCE 444 AA; 48490 MW; 882CFCCA89EF7DAF CRC64;

Query Match 49.3%; Score 1300.5; DB 2; Length 444;

Best Local Similarity 57.4%; Pred. No. 8.3e-80;

Matches 257; Conservativity 72; Mismatches 104; Indels 15; Gaps 6

QY 71 DVRLTLIEFMKDBEQGEFMQAEVAVASLQPVFEKRELL--PFFKQIVEERVITPVR 128

DB 3 DLNTLPANLKORNPQDEPFHOAVEEVFMSLDPFLANKKRYTQOSSLERIVERERVMPVR 62

QY 129 SWLDDAGNLQVNRGFRVQVSSAIGPYKGLRFPSPVNSIMKFLAFEOIFPKSLTTLTPMG 188

DB 63 TWQDDKQGVQVNRGRVQVMSAIGPYKGLRFPVTDGYLKLFLAFQVFKALATLTPMG 122

QY 189 GKGSGSDFDPKSGSDAEVWRFCQSPFMTELQHSISYVDVPADGIDVGAREIGYLFQYQR 248

DB 123 GKGSGSDFDPKSGSDAEVWRFCQSPFMTELQHSISYVDVPADGIDVGAREIGYLFQYQR 182

QY 249 ITKNYTVGLTFKQGEYGGSEIRPERATGAGVLPFENVLKDKGESLKGKCLVSGAGNVAQ 308

DB 183 IRNFFSSVLTGKGLEWGGSLIRPERATGAGVYFAQAMLTQTRNDSPEGRKVLVLSGSGNVAQ 242

QY 309 YCAELLEKGAGIVLSLSDSGYVEP--NGPFRLOLAQVODMKKKNNASIRSEYKSDTAVY 367

DB 243 YAAEKAIQLGAKVLTVDSDNSGFVLPPDSGMTBAQLAALTELKAVRR--RVATLYAKEQGLQ 301

QY 368 VGDRKKWEMLDQVDIAFPFCATONEIEHDAELLIKGCGQVVEGANNPSTNEAIHKYK 427


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Query Match      94.4%; Score 2489; DB 1; Length 523;
Best Local Similarity 96.8%; Pred. No. 3e-160;
Matches 486; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 11 VACAWRSARADYRAKAVASLEBQISAMDYTGDFALQAKVOMATKAGTEGLVHGKIP 70
DB 24 VACARBSAKRDVAAK--RLRSRSPMDATTDGFTLQAKVOMATKAGTEGLVHGKIP 81

QY 71 DVKQLLTETPMKDPBEOEFMOAVREVAVSLQPVFEKRPPELLPIFKQIVBERVITRVSM 130
DB 82 ELRQLLTETPMKDPBEOEFMOAVREVAVSLQPVFEKRPPELLPIFKQIVBERVITRVSM 141

QY 131 LDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMGGG 190
DB 142 LDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMGGG 201

QY 191 KGSDDPDKGKSDAEVWRFCQSPMTLORHISVYQDVPAGDIGVAREIGYLFQYKRTT 250
DB 202 KGSDDPDKGKSDAEVWRFCQSPMTLORHISVYQDVPAGDIGVAREIGYLFQYKRTT 261

QY 251 KNYTGLVLPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSGANVAQYC 310
DB 262 KNYTGLVLPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSGANVAQYC 321

QY 311 AELLLEKGAIVLSLSSQGYVVEPNFTREBQLOAVODMKKNNASISEKSTAYVGD 370
DB 322 AELLLEKGAIVLSLSSQGYVVEPNFTREBQLOAVODMKKNNASISEKSTAYVGD 381

QY 371 RRRKPEWLDQVDAIFPCATONEIDEHDAELLIKHGQYVVEGANMSTNEAIHKYNKAGI 430
DB 382 RRRKPEWLDQVDAIFPCATONEIDEHDAELLIKHGQYVVEGANMSTNEAIHKYNKAGI 441

QY 431 ITCPGKANAAGVAVSGLEMTQNRMSLNTWREVRDRLERIMKDIDYSAMGSPRRYVVDL 490
DB 442 ITCPGKANAAGVAVSGLEMTQNRMSLNTWREVRDRLERIMKDIDYSAMGSPRRYVVDL 501

QY 491 AAGANTAGFTKYADAVKAGAV 512
DB 502 AAGANTAGFTKYADAVKAGAV 523

RESULT 2
Q81LF7 PRELIMINARY; PRT; 510 AA.
AC Q81LF7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase, putative.
GN ORFNames=PF14_0286;
OS Plasmodium falciparum (isolate JD7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung B., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyse S.,
RA Chan M.S., Nene V., Shalimov S.J., Hafe D., Peterson J., Angiuoli S.,
RA Martin D.M., Fairclamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum.";
RL Nature 419:498-511(2002).
DR EMBL: AE014620; AAN36899.1; -.
DR HSSP: P24295; IAUJ.
DR GO: GO:0016491, F:oxidoreductase activity, IEA.
DR GO: GO:0006520, P:amino acid metabolism, IEA.
DR InterPro: IPR006095; GLFV_dehydrog.

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DR InterPro: IPR006096; GLFV_dehydrog_C.
DR InterPro: IPR006097; GLFV_dehydrog_N.
DR Pfam: PF00208; GLFV_dehydrog_1.
DR Pfam: PF02812; GLFV_dehydrog_N_1.
DR PRINTS: PR00082; GLFVDRGNASE.
DR PROSITE: PS00074; GLFV_DEHYDROGENASE_1.
SQ SEQUENCE 510 AA; 57343 MW; AC400045529AC64F CRC64;

Query Match      52.1%; Score 1375; DB 2; Length 510;
Best Local Similarity 60.0%; Pred. No. 8.9e-85;
Matches 267; Conservative 66; Mismatches 104; Indels 8; Gaps 5;

QY 72 VQQLLTETPMKDPBEOEFMOAVREVAVSLQPVFEKRPPELLPIFKQIVBERVITRVSM 131
DB 70 IELERKVSNNKNRPEFLQAEVLSCLKPVFKDNYIIGLENIABERVIOFRVPMI 129

QY 132 DDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMGGGK 191
DB 130 NKGEHKNNRGRVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMGGGK 189

QY 192 GGSDDPDKGKSDAEVWRFCQSPMTLORHISVYQDVPAGDIGVAREIGYLFQYKRTT 251
DB 190 GGSDDPDKGKSDAEVWRFCQSPMTLORHISVYQDVPAGDIGVAREIGYLFQYKRTT 249

QY 252 KNYTGLVLPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSGANVAQYC 311
DB 250 SPEGVLTKGNIKMGSGNIRAEATGYGVYFAENVLKDINDENKRCCLVSGANVAQYL 309

QY 312 EELLLEKGAIVLSLSSQGYVVEPNFTREBQLOAVODMKKNNASISEKSTAYVGD 369
DB 310 ELLIERKGAIVLSLSSQGYVVEPNFTREBQLOAVODMKKNNASISEKSTAYVGD 367

QY 370 DRRKPEWLDQVDAIFPCATONEIDEHDAELLIKHGQYVVEGANMSTNEAIHKYNKAG 429
DB 368 ENQKPEWNPIC--DIAPCATONEINENDADLFIQKKCKIVIGANNPTIHKALHKLQNN 425

QY 430 ITCPGKANAAGVAVSGLEMTQNRMSLNTWREVRDRLERIMKDIDYSAMGSPRRY--N 487
DB 426 ITCPSKANAGVAVSGLEMSQNSMRQWTHQETDMKLQNIKSIYEQCHNTSKTYLNE 485

QY 488 VDLAAGANTAGFTKYADAVKAGAV 512
DB 486 SDLVAGANTAGFLKVAADSLFLQGG 510

RESULT 3
Q7RQ39 PRELIMINARY; PRT; 1203 AA.
AC Q7RQ39;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=PY01264;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73339;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RX PubMed=12358865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Sun B.B., Kooij T.W., Petrea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalimov S.J., van Aken S.B., Riedmiller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Vates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:12:18 / Search time 92.6807 Seconds
(without alignments)
2828.902 Million cell updates/sec

Title: US-10-627-886-4

Perfect score: 2638
Sequence: 1 MOTALVAKPIVACAWRSK.....GANIAGPTVADAVKAGAV 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*
1: uniProt_sprot:*
2: uniProt_tmbl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2489	94.4	523	1 DHE4_CHISO	P28998 chloroella s
2	1375	52.1	2	081LF7	081LF7 plasmodium
3	1361	51.6	1203	2 07RO39	07RO39 plasmodium
4	1338	50.3	446	2 07YU9	07YU9 spironucleu
5	1327.5	50.3	449	2 07R3N7	07R3N7 giardia lam
6	1324.5	50.2	449	1 DHE3_GIALA	09HVJ7 pseudomonas
7	1309	49.6	445	2 09HVJ7	09HVJ7 pseudomonas
8	1300.5	49.3	444	2 09JY71	09JY71 neisseria m
9	1294.5	49.1	444	2 09JY56	09JY56 neisseria m
10	1287.5	48.8	449	2 088023	088023 pseudomonas
11	1286.5	48.8	470	2 096940	096940 plasmodium
12	1286.5	48.8	470	2 081LT0	081LT0 plasmodium
13	1285	48.7	445	2 0923C4	0923C4 pseudomonas
14	1284.5	48.7	437	2 07YZU7	07YZU7 trichomonas
15	1265	48.0	442	2 09TXS8	09TXS8 plasmodium
16	1264	47.9	442	2 09GTX5	09GTX5 plasmodium
17	1257	47.6	445	2 06S143	06S143 unculatured
18	1253.5	47.5	536	2 07RGT5	07RGT5 plasmodium
19	1250.5	47.4	448	2 086G10	086G10 bifidobacte
20	1250.5	47.4	445	2 086G72	086G72 ruminoococ
21	1249.5	47.4	447	2 06F67	06F67 actinobact
22	1241.5	47.1	448	2 08XK85	08XK85 clostridium
23	1240.5	47.0	449	2 0883U6	0883U6 streptococ
24	1239.5	47.0	448	2 0835G2	0835G2 enterococ
25	1238	46.9	449	1 DHE4_HAEIN	P43793 haemophilus
26	1236.5	46.9	449	2 08DY77	08DY77 streptococ
27	1234	46.8	447	2 061083	061083 trypanosoma
28	1231.5	46.7	442	2 06S57	06S57 manheimia
29	1230.5	46.6	449	2 08DUL2	08DUL2 streptococ
30	1230	46.6	449	2 09CPJ4	09CPJ4 pasteurella
31	1225.5	46.5	444	1 DHE3_BACTN	P94598 bacteroides

32	1225	46.4	448	2 09AIW1	09AIW1 streptococ
33	1214.5	46.0	444	1 DHE4_PRRU	P95544 prevotella
34	1214	45.9	448	2 08DGO	08DGO streptococ
35	1212	45.9	448	2 0970B4	0970B4 streptococ
36	1210.5	45.9	458	2 09KB34	09KB34 bacillus ha
37	1206.5	45.7	447	2 07VSN6	07VSN6 bordetella
38	1205.5	45.7	424	2 09RTN9	09RTN9 delnoco
39	1205.5	45.7	444	2 064081	064081 bacteroides
40	1205.5	45.7	464	2 07MEU7	07MEU7 bordetella
41	1202	45.6	448	2 088XM9	088XM9 iacobact
42	1201	45.5	447	1 DHE4_ECOLI	P00370 escherichia
43	1200.5	45.5	446	2 060996	060996 trypanosoma
44	1200	45.5	449	2 06AJB1	06AJB1 desulfocale
45	1199	45.5	443	2 097L29	097L29 clostridium

ALIGNMENTS

RESULT 1
DHE4_CHISO STANDARD; PRT; 523 AA.
ID P28998;
AC 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH) (Fragment).
OS Chloroella sorokiniana.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OX Chlorellaceae; Chloroella.
RN NCBI_TaxID=3076;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92032762; PubMed=1718478;
RA Cock J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;
RT "A nuclear gene with many introns encoding ammonium-inducible
RT chloroplastic NADP-specific glutamate dehydrogenase(s) in Chloroella
RT sorokiniana.";
RL Plant Mol. Biol. 17:1023-1044(1991).
CC -1- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate
CC + NH(3) + NADPH.
CC -1- SUBUNIT: Homo- and heterohexamer of alpha and beta subunits. Both
CC subunits are encoded by the same gene.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By ammonium.
CC -1- PTM: The N-termini of the alpha and the beta chains are blocked.
CC -1- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@eb-sib.ch).
CC -----
CC EMBL: X58832; CAA1636.1;
CC EMBL: X58831; CAA1635.1; ALT_SEQ.
CC PIR: S17949; S17949.
CC HSSP: P24295; IADP.
CC InterPro: IPR006095; GLFV_dehydrog.
CC InterPro: IPR006096; GLFV_dehydrog.C.
CC InterPro: IPR006097; GLFV_dehydrog.N.
CC Pfam: PF02018; GLFV_dehydrog.1.
CC Pfam: PF02812; GLFV_dehydrog.N.1.
CC PRINTS: PR00082; GLFVDRGNASE.
CC PROSITE: PS00074; GLFV_DEHYDROGENASE; 1.
CC Chloroplast; NADP; Oxidoreductase.
CC KM
CC FT
CC NON_TER 1
CC ACT_SITE 202
CC FT
CC SQ SEQUENCE 523 AA; 57529 MW; A35FE730E5FB974 CRC64;